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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:20:54 ; Search time 135 Seconds
(without alignments)
760.153 Million cell updates/sec

Title: US-09-825-212-1

Perfect score: 1662

Sequence: 1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1662	100.0	320	10	US-09-825-212-1
2	1593	95.8	312	9	US-09-925-637-14
3	1593	95.8	312	14	Sequence 14, Appl
4	1593	95.8	312	14	Sequence 14, Appl
5	1582	95.2	311	16	US-10-712-713-14
6	1561	93.9	311	16	US-10-787-887-2
7	1452	87.4	310	16	US-10-032-201B-265
8	1154	69.4	315	12	US-10-787-887-10
9	1154	69.4	315	12	US-10-290-072-66
10	1154	69.4	315	14	US-10-141-531-66
11	1145.5	68.9	315	14	US-10-032-201B-198
12	1145.5	68.9	315	12	US-10-032-201B-235
13	1145	68.9	316	12	US-10-290-072-103
14	1145	68.9	316	12	US-10-290-072-139
15	1145	68.9	316	14	US-10-141-531-103
					Sequence 139, Appl

16	1144	68.8	316	12	US-10-290-072-148	Sequence 148, App
17	1144	68.8	316	14	US-10-141-531-148	Sequence 148, App
18	1143	68.8	316	12	US-10-290-072-85	Sequence 85, App
19	1143	68.8	316	12	US-10-290-072-130	Sequence 130, App
20	1143	68.8	316	14	US-10-141-531-85	Sequence 85, Appl
21	1143	68.8	316	14	US-10-141-531-130	Sequence 130, App
22	1141	68.7	316	12	US-10-290-072-184	Sequence 184, App
23	1141	68.7	316	14	US-10-141-531-184	Sequence 184, App
24	1137	68.4	316	12	US-10-290-072-112	Sequence 112, App
25	1137	68.4	316	12	US-10-290-072-157	Sequence 157, App
26	1137	68.4	316	14	US-10-141-531-112	Sequence 112, App
27	1137	68.4	316	14	US-10-141-531-157	Sequence 157, App
28	1137	68.4	316	14	US-10-141-531-175	Sequence 175, App
29	1137	68.4	316	12	US-10-290-072-94	Sequence 94, Appl
30	1136	68.4	316	12	US-10-290-072-121	Sequence 121, App
31	1136	68.4	316	12	US-10-290-072-193	Sequence 193, App
32	1136	68.4	316	14	US-10-141-531-94	Sequence 94, Appl
33	1136	68.4	316	14	US-10-141-531-121	Sequence 121, App
34	1136	68.4	316	14	US-10-141-531-166	Sequence 166, App
35	1136	68.4	316	14	US-10-141-531-202	Sequence 202, App
36	1135	68.3	316	14	US-10-032-201B-212	Sequence 212, App
37	1135	68.3	316	14	US-10-032-201B-253	Sequence 253, App
38	1134	68.2	316	14	US-10-032-201B-268	Sequence 268, App
39	1134	68.2	316	14	US-10-032-201B-244	Sequence 244, App
40	1054	63.4	319	14	US-10-032-201B-208	Sequence 208, App
41	872	52.5	308	14	US-10-032-201B-212	
42	849	51.1	303	14	US-10-032-201B-268	
43	753	45.3	314	14	US-10-032-201B-244	
44	728.5	43.8	325	14	US-10-032-201B-244	
45	726	43.7	315	14	US-10-032-201B-208	

ALIGNMENTS

RESULT 1

US-09-825-212-1
; Sequence 1, Application US/09825212
; Publication No. US20030166843A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Timothy E
; TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF STAPHYLOCOCCUS AUREUS THIOREDOXIN REDUCTASE
; FILE REFERENCE: 00032.US1
; CURRENT APPLICATION NUMBER: US/09/825,212
; PRIOR APPLICATION NUMBER: 2001-04-03
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-825-212-1

Query Match 100.0%; Score 1662; DB 10; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.5e+148;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPFGFEMIT 60	
DB	1	MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENPFGFEMIT 60	
QY	61	GPDLSTKMFHAKKPGAVYQVDIKSVKDGKYEKVINFGNKELTAKAVIATGASYKKIG 120	
DB	61	GPDLSTKMFHAKKPGAVYQVDIKSVKDGKYEKVINFGNKELTAKAVIATGASYKKIG 120	
QY	121	VPGEELGGRGVSYCAVCDGAFFKNNKRLFVIGGDSAAVEEGTFTTKFADKVTIVHRRDEL 180	
DB	121	VPGEELGGRGVSYCAVCDGAFFKNNKRLFVIGGDSAAVEEGTFTTKFADKVTIVHRRDEL 180	
QY	181	RAQRILQDRAFNKIDFINSHHTYSINEKDGKGSVTLTSTKDGSEETHEADGVFIYIG 240	

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Db 181 RAQRILQDRAFNKDKIDFWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYIG 240
QY 241 MKPLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
Db 241 MKPLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
QY 301 AAAYIEHLNDQARSHHHH 320
Db 301 AAAYIEHLNDQARSHHHH 320

RESULT 2
US-09-925-637-14
; Sequence 14, Application US/09925637
; Patent No. US2002010338A1
; GENERAL INFORMATION:
; APPLICANT: Choi
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
; FILE REFERENCE: PB560
; CURRENT APPLICATION NUMBER: US/09/925,637
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/151,933
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 08/781,986
; PRIOR FILING DATE: 1997-01-03
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-637-14
Query Match 95.8%; Score 1593; DB 9; Length 312;
Best Local Similarity 99.4%; Pred. No. 1.7e-141;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPFEMIT 60
Db 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPFEMIT 60
QY 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKXIG 120
Db 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKXIG 120
QY 121 VPGEQELGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDEL 180
Db 121 VPGEQELGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDEL 180
QY 181 RAQRILQDRAFNKDKIDFWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYIG 240
Db 181 RAQRILQDRAFNKDKIDFWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYIG 240
QY 241 MKPLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
Db 241 MKPLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
QY 301 AAAYIEHLNDQAR 312
Db 301 AAAYIEHLNDQAR 312

RESULT 3
US-10-084-205-14
; Sequence 14, Application US/10084205
; Publication No. US20030049648A1
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; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: PB515P1
; CURRENT APPLICATION NUMBER: US/10/084,205
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 14
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-084-205-14
Query Match 95.8%; Score 1593; DB 14; Length 312;
Best Local Similarity 99.4%; Pred. No. 1.7e-141;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPFEMIT 60
Db 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPFEMIT 60
QY 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKXIG 120
Db 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKXIG 120
QY 121 VPGEQELGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDEL 180
Db 121 VPGEQELGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDEL 180
QY 181 RAQRILQDRAFNKDKIDFWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYIG 240
Db 181 RAQRILQDRAFNKDKIDFWSHTTKSINEKDGKGVSVTLSTKDGSEETHADGVFIYIG 240
QY 241 MKPLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
Db 241 MKPLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQS 300
QY 301 AAAYIEHLNDQAR 312
Db 301 AAAYIEHLNDQAR 312

RESULT 4
US-10-712-713-14
; Sequence 14, Application US/10712713
; Publication No. US20040082002A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: PB515P1
; CURRENT APPLICATION NUMBER: US/10/712,713
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/084,205
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/151,933
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 14
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-712-713-14
Query Match 95.8%; Score 1593; DB 16; Length 312;
Best Local Similarity 99.4%; Pred. No. 1.7e-141;
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Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGTEIDFDIALIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMIT 60
 Db 1 MGTEIDFDIALIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMIT 60

Qy 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKNELTAKAVIIATGAAYKKIG 120
 Db 61 GPDLSKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKNELTAKAVIIATGAAYKKIG 120

Qy 121 VPGEQLGGRGVSYCAVCDGAFKKNKELFVIGGGDSAVEEGTFTTKFADKVTIIVHRRDEL 180
 Db 121 VPGEQLGGRGVSYCAVCDGAFKKNKELFVIGGGDSAVEEGTFTTKFADKVTIIVHRRDEL 180

Qy 181 RAQRILODRAFKNKDIFWHSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIG 240
 Db 181 RAQRILODRAFKNKDIFWHSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIG 240

Qy 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGDVDRDKGLRQIVTATGDSIAAQS 300
 Db 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGDVDRDKGLRQIVTATGDSIAAQS 300

Qy 301 AAEYIEHLNDQA 312
 Db 301 AAEYIEHLNDQA 312

RESULT 5

US-10-787-887-2
 ; Sequence 2, Application US/10787887
 ; Publication No. US20040161809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aharonowitz, Yair
 ; APPLICANT: Borovok, Ilya
 ; APPLICANT: Cohen, Gerald
 ; APPLICANT: Uziel, Orit
 ; APPLICANT: Katz, Leonard
 ; TITLE OF INVENTION: Recombinant Staphylococcus Thioresoxin Reductase
 ; FILE REFERENCE: 85189-899
 ; CURRENT APPLICATION NUMBER: US/10/787,887
 ; CURRENT FILING DATE: 2004-02-27
 ; PRIOR APPLICATION NUMBER: US 60/076,525
 ; PRIOR FILING DATE: 1998-03-02
 ; PRIOR APPLICATION NUMBER: US 09/261,301
 ; PRIOR FILING DATE: 1999-03-02
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-10-787-887-2

Query Match 95.2%; Score 1582; DB 16; Length 311;
 Best Local Similarity 99.4%; Pred. No. 1.8e-140;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TEIDFDIALIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMITGP 62
 Db 2 TEIDFDIALIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMITGP 61

Qy 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKNELTAKAVIIATGAAYKKIGVP 122
 Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKNELTAKAVIIATGAAYKKIGVP 121

Qy 123 GEQELGGRGVSYCAVCDGAFKKNKELFVIGGGDSAVEEGTFTTKFADKVTIIVHRRDELRA 182
 Db 122 GEQELGGRGVSYCAVCDGAFKKNKELFVIGGGDSAVEEGTFTTKFADKVTIIVHRRDELRA 181

Qy 183 QRILQDRAFKNKDIFWHSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIGMK 242
 Db 182 QRILQDRAFKNKDIFWHSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIGMK 241

RESULT 7

US-10-787-887-10
 ; Sequence 10, Application US/10787887
 ; Publication No. US20040161809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aharonowitz, Yair
 ; APPLICANT: Borovok, Ilya
 ; APPLICANT: Cohen, Gerald
 ; APPLICANT: Uziel, Orit

Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGDVDRDKGLRQIVTATGDSIAAQSAA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGDVDRDKGLRQIVTATGDSIAAQSAA 301

Qy 303 EYIEHLNDQA 312
 Db 302 EYIEHLNDQA 311

RESULT 6
 US-10-032-201B-265
 ; Sequence 265, Application US/10032201B
 ; Publication No. US20030167524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Rooijen, Gijb
 ; APPLICANT: Deckers, Harm
 ; APPLICANT: Heifetz, Peter Bernard
 ; APPLICANT: Briggs, Steven
 ; APPLICANT: Dalmia, Bipin Kumar
 ; APPLICANT: Del Val, Greg
 ; APPLICANT: Zaplachinski, Steve
 ; APPLICANT: Moloney, Maurice
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
 ; FILE REFERENCE: 38814 351B
 ; CURRENT APPLICATION NUMBER: US/10/032,201B
 ; CURRENT FILING DATE: 2001-12-19
 ; NUMBER OF SEQ ID NOS: 313
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 265
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-10-032-201B-265

Query Match 93.9%; Score 1561; DB 14; Length 311;
 Best Local Similarity 98.1%; Pred. No. 1.7e-138;
 Matches 304; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TEIDFDIALIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMITGP 62
 Db 2 TEIDFDIALIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNPFGEFMITGP 61

Qy 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKNELTAKAVIIATGAAYKKIGVP 122
 Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKNELTAKAVIIATGAAYKKIGVP 121

Qy 123 GEQELGGRGVSYCAVCDGAFKKNKELFVIGGGDSAVEEGTFTTKFADKVTIIVHRRDELRA 182
 Db 122 GEQELGGRGVSYCAVCDGAFKKNKELFVIGGGDSAVEEGTFTTKFADKVTIIVHRRDELRA 181

Qy 183 QRILQDRAFKNKDIFWHSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIGMK 242
 Db 182 QRILQDRAFKNKDIFWHSHTTKSINEXDKGVSVTLTSTKDGSETHADGVFIYIGMK 241

Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGDVDRDKGLRQIVTATGDSIAAQSAA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGDVDRDKGLRQIVTATGDSIAAQSAA 301

Qy 303 EYIEHLNDQA 312
 Db 302 EYIEHLNDQA 311

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; APPLICANT: Katz, Leonard
; TITLE OF INVENTION: Recombinant Staphylococcus Thioredoxin Reductase
; FILE REFERENCE: 85189-899
; CURRENT APPLICATION NUMBER: US/10/787,887
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/076,525
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: US 09/261,301
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-787-887-10

Query Match      87.4%; Score 1452; DB 16; Length 310;
Best Local Similarity 89.9%; Pred. No. 3.2e-128;
Matches 277; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 3 TEIDFDIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP 62
Db 2 TEVDFVAILIAGPAGMTAAVYASRANLKTVMIERGMPGGQMANTEEVENFPGFEMITGP 61
QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAKAVIIATGAAYKKIGV 122
Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINLGNKEITAHAVIISTGAAYKKIGV 121
QY 123 GEQLGGRGVSVCADGAFKFNKRLFVIGGDSAVBEGTFTTKFADKVTIVHRRDLRA 182
Db 122 GEQLGGRGVSVCADGAFKFNKRLFVIGGDSAVBEGTFTTKFADKVTIVHRRDLRA 181
QY 183 QRILQDRAFNKDKIDFTWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
Db 182 QNIIQERAFNKDKVDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 241
QY 243 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQA 302
Db 242 PLTAPFKNLGINTDAGYIVTQDDMTSKVRGIFAAGDVRDKGLRQIVTATGDSIAAQA 301
QY 303 EYIEHLND 310
Db 302 DYITELKD 309

RESULT 8
US-10-290-072-66
; Sequence 66, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
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; LENGTH: 315
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-290-072-66

Query Match      69.4%; Score 1154; DB 12; Length 315;
Best Local Similarity 71.4%; Pred. No. 3.9e-100;
Matches 220; Conservative 33; Mismatches 55; Indels 0; Gaps 0;

QY 7 FDIATIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLS 66
Db 6 YDVIITIGAGPAGMTAAVYTSRANLSTLMIERGIPGGQMANTEDVENYPGFESILGPELS 65
QY 67 KMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAKAVIIATGAAYKKIGVPEQE 126
Db 66 KMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAKAVIIATGAAYKKIGVPEQE 125
QY 127 LGGRGVSVCADGAFKFNKRLFVIGGDSAVBEGTFTTKFADKVTIVHRRDLRAQRI 186
Db 126 LGGRGVSVCADGAFKFNKRLFVIGGDSAVBEGTFTTKFADKVTIVHRRDLRAQRI 185
QY 187 QDRAFNKDKIDFTWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
Db 186 QARAFDNEKVDLWNTVKEIHEENGKVGNTLVDTVTGSESEFKTDGVFIYIGMLPLSK 245
QY 247 PFKDLGITNDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQAABYIE 306
Db 246 PFENLGITNEEGVIEINDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQAQSVQHYVE 305
QY 307 HLNDQARS 314
Db 306 ELQETLTK 313

RESULT 9
US-10-141-531-66
; Sequence 66, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Lugimbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-141-531-66

Query Match      69.4%; Score 1154; DB 14; Length 315;
Best Local Similarity 71.4%; Pred. No. 3.9e-100;
Matches 220; Conservative 33; Mismatches 55; Indels 0; Gaps 0;

QY 7 FDIATIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLS 66
Db 6 YDVIITIGAGPAGMTAAVYTSRANLSTLMIERGIPGGQMANTEDVENYPGFESILGPELS 65
QY 67 KMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAKAVIIATGAAYKKIGVPEQE 126
Db 66 KMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKLTAKAVIIATGAAYKKIGVPEQE 125
```

Query Match	69.4%;	Score 1154;	DB 14;	Length 315;
Best Local Similarity	71.4%;	Pred. No. 3.9e-100;		
Matches 220;	Conservative 33;	Mismatches 55;	Indels 0;	Gaps 0;
QY	7	FDIAIIGAGPAGTAAVAYSRANLKIVMTIERGIPGGOMANTEVENPPGEMITGPDLSLT	66	
Ddb	6	YDVIIIGAGPAGTAAVYTSRANLSTLMTIERGIPGGQMANTVEDVNPYGESILGPESLN	65	
QY	67	KMFHAKKFGAVQYGDIIKSVDKGEYKVINFGNKELTAKAVIIATCAEYKKIIVGPGQEQE	126	
Ddb	66	KMFHAKKFGAEVAGDIIKEVIDGKEYKVVKAGSKKEYKARAVIIAAGAEYKKIIVGPGKEK	125	
QY	127	LGGRGVSYCAVCDGAPFFKNKRLFVIGGDSAVEEGTFTTKFADKVIIVHRRDELRAQRIL	186	
Ddb	126	LGGRGVSYCAVCDGAPFFKGLVAVVGGDGSAVEEGVYLTRFASKVITRVHRRDKLRAQSIL	185	
QY	187	QDRAFNDKIDFIWSHTTKSINEKQGVGSVILSTKDGSEETHADGVFIYIGMKPLTA	246	
Ddb	186	QARAFDNEKVDLWNNKTVEIHEENGKGVNLTVDVTGTGESEFETDGVFIYIGMLPLSK	245	
QY	247	PPKDLGITNDVGXIYITKDDMTTSVPGIFAAGDVDRDKGLRQIVTATGDSGTAAQSAAEYTE	306	
Ddb	246	PPENLGITNEEGYIENDRMTKEVGIIPAAGDIREKSLRQIVTATGDSIAAQSVQHYVE	305	
QY	307	HLNDQARS	314	
Ddb	306	ELQETLKT	313	

RESULT 12
US-10-290-072-103
/ Sequence 103, Application US/10290072
/ Publication No. US2003021151A1
/ GENERAL INFORMATION:
/ APPLICANT: Briggs, Steven P.
/ APPLICANT: Dalmida, Bipin K.
/ APPLICANT: del Val, Greg
/ APPLICANT: Desjarlais, John R.
/ APPLICANT: Heifetz, Peter
/ APPLICANT: Luginbuhl, Peter
/ APPLICANT: Muchhal, Umesh
/ TITLE OF INVENTION: Nucleic Acids and
/ FILE REFERENCE: A-71457-3
/ CURRENT APPLICATION NUMBER: US/10/290-072-103
/ CURRENT FILING DATE: 2002-11-06
/ PRIOR APPLICATION NUMBER: US 60/370,610
/ PRIOR FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: US 60/376,682
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 10/141,531
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PatentIn version 3.2
SEQ ID NO 103
LENGTH: 316
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Bacillus subtilis variant
US-10-290-072-103
Query Match 68.9%; Score 1145; DB 12; Length 316;
Best Local Similarity 70.1%; Pred. No. 2.8e-99;
Matches 220; Conservative 33; Mismatches 61; Indels 0; Gaps 0;
QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPPGEMIT 60
Db 1 MSEEKIYDVIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGOMANTEVENPPGESIL 60
QY 61 GPDLSKTMFEHAKKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIIATGAEYKIG 120
Db 61 GPESLNKMFHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKIG 120
QY 121 VPGEQLGGRGVSYCAVCDGAPFFKNKRLFVIGGDSAVEEGTFTTKPADKVTIVHRRDEL 180
Db 121 VPGEKELGGRGVSYCAVCDGAPFFKGKELVVGGSADSAVERGVYLTFRFASKVTIVHRYDKL 180
QY 181 RAQRILQDRAFDKIDFINSHTTKSINEKDGKGVSVTLSTKDGSETHADGVFIYIG 240
Db 181 NAQSILQARAFDNEKVDLWNTKVKETHEENGKVGNNVLTVDVTGSESEFKTDGVFIYIG 240
QY 241 MKPLTAPFKDLGINDVGYITVKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQS 300
Db 241 MLPLSKPFENIGITNEEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQS 300
QY 301 AAETIEHLNDQARS 314
Db 301 VQHVVEELQETLKT 314
RESULT 13
US-10-290-072-139
Sequence 139, Application US/10290072
Publication No. US20030211511A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Luginbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: A-71457-3
CURRENT FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/376,682
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 10/141,531
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PatentIn version 3.2
SEQ ID NO 139
LENGTH: 316

TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Bacillus subtilis variant
US-10-290-072-139
Query Match 68.9%; Score 1145; DB 12; Length 316;
Best Local Similarity 70.1%; Pred. No. 2.8e-99;
Matches 220; Conservative 33; Mismatches 61; Indels 0; Gaps 0;
QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPPGEMIT 60
Db 1 MSEEKIYDVIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGOMANTEVENPPGESIL 60
QY 61 GPDLSKTMFEHAKKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIIATGAEYKIG 120
Db 61 GPESLNKMFHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKIG 120
QY 121 VPGEQLGGRGVSYCAVCDGAPFFKNKRLFVIGGDSAVEEGTFTTKPADKVTIVHRRDEL 180
Db 121 VPGEKELGGRGVSYCAVCDGAPFFKGKELVVGGSADSAVERGVYLTFRFASKVTIVHRYDKL 180
QY 181 RAQRILQDRAFDKIDFINSHTTKSINEKDGKGVSVTLSTKDGSETHADGVFIYIG 240
Db 181 NAQSILQARAFDNEKVDLWNTKVKETHEENGKVGNNVLTVDVTGSESEFKTDGVFIYIG 240
QY 241 MKPLTAPFKDLGINDVGYITVKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQS 300
Db 241 MLPLSKPFENIGITNEEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQS 300
QY 301 AAETIEHLNDQARS 314
Db 301 VQHVVEELQETLKT 314
RESULT 14
US-10-141-531-103
Sequence 103, Application US/10141531
Publication No. US20030100743A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: del Val, Greg
APPLICANT: Desjarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Luginbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: A-71457-2/RET/RMS/RMK
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US 60/370,609
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/289,029
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn version 3.1
SEQ ID NO 103
LENGTH: 316
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Bacillus subtilis variant
US-10-141-531-103
Query Match 68.9%; Score 1145; DB 14; Length 316;
Best Local Similarity 70.1%; Pred. No. 2.8e-99;
Matches 220; Conservative 33; Mismatches 61; Indels 0; Gaps 0;
QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPPGEMIT 60
Db 1 MSEEKIYDVIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGOMANTEVENPPGESIL 60

QY 61 GPDISTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKKELTAKAVIATGAEEKIG 120
Db 61 GPELSNKMFEHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIINAGAEYKIG 120
QY 121 VPGQELGGRGVSYCAVCDGAFKFKKL FVIGGGDSAVEEGTFTTKPADKVTIVHRRDEL 180
Db 121 VPGQELGGRGVSYCAVCDGAFKFKKL FVIGGGDSAVEEGTFTTKPADKVTIVHRRDEL 180
QY 181 RAQRILQDRAFKNDKIDFIWSTTKSINBKDGKGVSVTLTSTKDGSEETHEADGVFIYIG 240
Db 181 NAQSILQARAFDNKVDLWNTKVEIHEENGKVGNNVLDVTVTGESEFKTDGVFIYIG 240
QY 241 MKPLTAPKDLGINDVGYIVTKDDMTTSVPGIPAAAGDVRDKGLRQIVTATGDSIAAQS 300
Db 241 MLPLSKFPENLGIETNEEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQS 300
QY 301 AAEYIEHLNDOARS 314
Db 301 VQHYVEELQETLKT 314

RESULT 15
US-10-141-531-139
; Sequence 139, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioresdoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Bacillus subtilis variant
US-10-141-531-139

Query Match 68.9%; Score 1145; DB 14; Length 316;
Best Local Similarity 70.1%; Pred. No. 2.8e-99;
Matches 220; Conservative 33; Mismatches 61; Indels 0; Gaps 0;
QY 1 MGTEDFDIATGAGPAGTAAYASRANLKTVMIERGIPGGQMANTEVENPFGPEMIT 60
Db 1 MGEEXIYDVIITGAGPAGTAAYTSRANLSTLMIERGIPGGQMANTEVENPFGPESIL 60
QY 61 GPDISTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKKELTAKAVIATGAEEKIG 120
Db 61 GPELSNKMFEHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIINAGAEYKIG 120
QY 121 VPGQELGGRGVSYCAVCDGAFKFKKL FVIGGGDSAVEEGTFTTKPADKVTIVHRRDEL 180
Db 121 VPGQELGGRGVSYCAVCDGAFKFKKL FVIGGGDSAVEEGTFTTKPADKVTIVHRRDEL 180
QY 181 RAQRILQDRAFKNDKIDFIWSTTKSINBKDGKGVSVTLTSTKDGSEETHEADGVFIYIG 240
Db 181 NAQSILQARAFDNKVDLWNTKVEIHEENGKVGNNVLDVTVTGESEFKTDGVFIYIG 240
QY 241 MKPLTAPKDLGINDVGYIVTKDDMTTSVPGIPAAAGDVRDKGLRQIVTATGDSIAAQS 300
Db 241 MLPLSKFPENLGIETNEEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQS 300

Db 241 MLPLSKFPENLGIETNEEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDSIAAQS 300
QY 301 AAEYIEHLNDOARS 314
Db 301 VQHYVEELQETLKT 314
Search completed: September 15, 2004, 12:32:46
Job time : 136 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:16:13 ; Search time 32 Seconds
(without alignments)
516.260 Million cell updates/sec

Title: US-09-825-212-1

Perfect score: 1662

Sequence: 1 MGTEIDFDIAIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1083	65.2	253	4	US-09-134-001C-5512
2	940	56.6	310	4	US-09-134-000C-5514
3	618	37.2	317	4	US-09-328-352-8114
4	607	36.5	320	4	US-09-328-352-5678
5	594	35.7	311	4	US-09-198-452A-331
6	581	35.0	339	4	US-09-543-681A-5633
7	579.5	34.9	333	4	US-09-598-747-25
8	575	34.6	300	4	US-09-598-747-7
9	571.5	34.4	329	4	US-09-134-000C-3897
10	565.5	34.3	321	4	US-09-540-014-25
11	568.5	34.2	349	4	US-09-489-039A-12096
12	559	33.6	332	4	US-09-540-014-24
13	549.5	33.1	323	4	US-09-252-991A-29849
14	524.5	31.6	332	4	US-09-540-014-9
15	513.5	30.9	334	1	US-08-386-729A-7
16	497.5	29.9	310	4	US-09-598-747-27
17	484.5	29.2	301	4	US-09-598-747-6
18	482	29.0	510	1	US-08-220-677A-2
19	455	27.4	522	4	US-09-252-991A-28463
20	454	27.3	523	4	US-09-328-352-6394
21	454	27.3	523	4	US-09-328-352-6395
22	449.5	27.0	524	4	US-09-540-236-2706
23	443	26.7	508	4	US-09-134-001C-4570
24	436	26.2	512	4	US-09-107-532A-6559
25	415	25.0	538	4	US-09-543-681A-4490
26	369.5	22.2	87	4	US-09-134-001C-5497
27	300.5	18.1	339	4	US-09-107-532A-6420

28	285.5	17.2	199	4	US-09-252-991A-31441	Sequence 31441, A
29	279	16.8	215	4	US-09-252-991A-31700	Sequence 31700, A
30	273	16.4	192	4	US-09-489-039A-13402	Sequence 13402, A
31	253	15.2	553	4	US-09-134-001C-2974	Sequence 2974, Ap
32	238	14.3	334	4	US-09-134-000C-5068	Sequence 5068, Ap
33	234	14.1	507	4	US-09-091-097-34	Sequence 34, Appl
34	233	14.0	507	4	US-09-091-097-10	Sequence 10, Appl
35	225	13.5	474	4	US-09-556-877-90	Sequence 90, Appl
36	225	13.5	474	4	US-09-620-412C-90	Sequence 90, Appl
37	225	13.5	474	4	US-09-410-568-90	Sequence 90, Appl
38	225	13.5	474	4	US-09-598-419-90	Sequence 90, Appl
39	218.5	13.1	496	4	US-09-328-352-6168	Sequence 6168, Ap
40	215	12.9	456	4	US-09-252-991A-28041	Sequence 28041, A
41	212	12.8	491	4	US-09-262-856A-5	Sequence 5, Appl
42	210	12.6	473	4	US-09-134-001C-3405	Sequence 3405, Ap
43	210	12.6	473	4	US-09-252-991A-25982	Sequence 25982, A
44	204	12.3	480	4	US-09-252-991A-32853	Sequence 32853, A
45	199	12.0	484	4	US-09-543-681A-5905	Sequence 5905, Ap

ALIGNMENTS

RESULT 1

US-09-134-001C-5512
; Sequence 5512, Application US/09134001C
; Patent No. 6380370

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 5512

; LENGTH: 253

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5512

Query Match

Best Local Similarity 65.2%; Score 1083; DB 4; Length 253;

Matches 209; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 67 KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFGNKKELTAKAVIATGAEYKKIGVPGQE 126

Db 9 KCLNMLKNLVAEYQYGDIKSVEDKGEYKVINFGNKKELTAKAVIATGAEYKKIGVPGQE 68

QY 127 LGGRGVSYCAVCDGAFFKKNKELFVIGGDSAVESGTFKTKADKVTIVHRRDELRAQIL 186

Db 69 LGGRGVSYCAVCDGAFFKKNKELFVIGGDSAVESGTFKTKADKVTIVHRRDELRAQIL 128

QY 187 QDRAPKNDKIDFIWSHTTKTSINEKDKGVSVTLTSTDKGSBETHADGVFIYIGMKPLTA 246

Db 129 QERAFKNDKIDFIWSHTTKTSINEKDKGVSVTLTSTDKGSBETHADGVFIYIGMKPLTA 188

QY 247 PFKDLGTNDVGYIVTKDDMTSTVPFIAGDVRDKGLRQIVTATDGSIAQAASAEYIE 306

Db 189 PFKNLGTNDVGYIVTKDDMTSTVPFIAGDVRDKGLRQIVTATDGSIAQAASAEYIE 248

QY 307 HLND 310

Db 249 ELKD 252

RESULT 2

US-09-134-000C-5514

; Sequence 5514, Application US/09134000C

Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5514
LENGTH: 310
TYPE: PR
ORGANISM: Enterococcus faecalis
US-09-134-000C-5514

Query Match 56.8%; Score 940; DB 4; Length 310;
Best Local Similarity 58.9%; Pred. No. 1.4e-85;
Matches 178; Conservative 42; Mismatches 82; Indels 0; Gaps 0;

QY 7 FDIATGAGPAGMTAAVYASRANKLKTVMIERGIPGGOMANTEEVENPPGFEMITGPDLSK 66
DB 8 YDVIILGAGPAGMTAAVYASRANKLKTVMIERGIPGGOMANTEEVENPPGDSIMGPCLAY 67

QY 67 KMEHAKFGAVYQYGDIKSVDEKGYKVINFGNKGELTAKAVIATGAEYKKGIVPGQEL 126
DB 68 KMYENVKFGTGNAYGIWGIEDHGSYKVICDDKSYEAKAVIATGCEHKLGVKGE 127

QY 127 LGRGVSVCVDCGAFKPKRLFVIGGDSAVEGFTTKFADKVTIVHRRDLRAQRI 186
DB 128 FAGRGVSVCVDCGAFKPKRLFVIGGDSAVEGFTTKFADKVTIVHRRDLRAQRI 187

QY 187 QDRAFNKDKIDFTWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
DB 188 QDRAFAANEKISFVWDTVBEIVGNEMVTVGVKARNVKTDEVSEIEANGVFIYVGLDPLTE 247

QY 247 PFKDLGNTDVGIVTKDDMTTSVPGIFAGDVDRKGLRQIVATGDSIAAQSAAYIE 306
DB 248 PFKAGITNAGMTIETQEMRTKIPVYAGDVDRKGLRQIVATGDSIAAQSAAYIE 307

QY 307 HL 308
DB 308 EL 309

RESULT 3
US-09-328-352-8114
Sequence 8114, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8114
LENGTH: 317
TYPE: PR
ORGANISM: Acinetobacter baumannii
US-09-328-352-8114

Query Match 37.2%; Score 618; DB 4; Length 317;
Best Local Similarity 44.1%; Pred. No. 1.9e-53;
Matches 137; Conservative 53; Mismatches 111; Indels 10; Gaps 4;

QY 9 IAIIGAGPAGMTAAVYASRANKLKTVMIERGIPGGOMANTEEVENPPGF-EMITGPDLSK 67
DB 8 LIILGSGPAGYSAVYAAARANKLPTLIAGLQGLQGLTTTTEVDNPNWPGDPEGLTGALMDR 67

QY 68 MFEHAKFGAVYQYGDIKSVDEKGYKVINFGNKGELTAKAVIATGAEYKKGIVPGQEL 127
DB 68 MQAHERFGTELVDYHINEVDLNVFPFVLKGMEEVTCDAIIATGATAQYLGSEQNF 127

QY 128 GGRGVSVCVDCGAFKPKRLFVIGGDSAVEGFTTKFADKVTIVHRRDLRAQRI 187
DB 128 MQQGVSAACATCDGFFYKQKQVMVGGNTAVEEALYLSNIAHSHVTLVHRRDLRSEKILQ 187

QY 188 DRAF---KNDKIDFTWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPL 244
DB 188 DHLFVKEKEGKISIIWNHEVEVLGDTGTGTVRLKSTODESKQDVEVHGLFVAIGYKPN 247

QY 245 TAPFKDLGNTDVGIVTKDDMT-----TSVPGIFAGDVDRKGLRQIVATGDSIAAQ 299
DB 248 TGMF-DGQLNLRDGIYQVSGTSGNATATSVAGVFAAGDVADSIYQAITSGAGGMAAL 306

QY 300 SAAEYIEHLND 310
DB 307 DAEKYLQDND 317

RESULT 4
US-09-328-352-5678
Sequence 5678, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5678
LENGTH: 320
TYPE: PR
ORGANISM: Acinetobacter baumannii
US-09-328-352-5678

Query Match 36.5%; Score 607; DB 4; Length 320;
Best Local Similarity 43.4%; Pred. No. 2.4e-52;
Matches 134; Conservative 55; Mismatches 110; Indels 10; Gaps 4;

QY 9 IAIIGAGPAGMTAAVYASRANKLKTVMIERGIPGGOMANTEEVENPPGF-EMITGPDLSK 67
DB 13 LIILGSGPAGYSAVYAAARANKLPTLIAGLQGLQGLTTTTEVDNPNWPGDPEGLTGALMDR 72

QY 68 MFEHAKFGAVYQYGDIKSVDEKGYKVINFGNKGELTAKAVIATGAEYKKGIVPGQEL 127
DB 73 MQAHERFGTELVDYHINEVDLNVFPFVLKGMDEYTCDAIIATGATAQYLGSEBQKF 132

QY 128 GGRGVSVCVDCGAFKPKRLFVIGGDSAVEGFTTKFADKVTIVHRRDLRAQRI 187
DB 133 MQQGVSAACATCDGFFYKQKQVMVGGNTAVEEALYLSNIAHSHVTLVHRRDLRSEKILQ 192

QY 188 DRAF---KNDKIDFTWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPL 244
DB 193 DHLFAKEKEGKISIIWNHEVEVLGDTGTGTVRLKSTODESKQDVEVHGLFVAIGYKPN 252

QY 245 TAPFKDLGNTDVGIVTKDDMT-----TSVPGIFAGDVDRKGLRQIVATGDSIAAQ 299
DB 253 TSMFEGQLNLRD-GYIQVSGTSGNATATSVAGVFAAGDVADSIYQAITSGAGGMAAL 311

QY 300 SAAEYIEHL 308
DB 312 DAEKYLQDND 320

RESULT 5
US-09-198-452A-331
Sequence 331, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:

[illegible]

RESULT 8
US-09-598-747-7
; Sequence 7, Application US/09598747
; Patent No. 6531648

```

; GENERAL INFORMATION:
; APPLICANT: Lanahan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Archaeoglobus fulgidus
US-09-598-747-7

Query Match          34.6%; Score 575; DB 4; Length 300;
Best Local Similarity 43.2%; Pred. No. 3.4e-49;
Matches 130; Conservative 53; Mismatches 112; Indels 6; Gaps 6;

QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPFGFEMITGPDLS 66
DB 2 YDVAIIGGAGLTAALYSARYGLKTVFFETVDPVSLSLAAKIENYVPGFEG-SGMELLE 60
QY 67 KMFEHAKKFGAVYQYGDIKSVDEKGE-YKVINFGNKELTAKAVIIATGAAYKKIGVPEQ 125
DB 61 KMKEQAVKAGAEKWLKVERVNERGETFTVIAEGG-EYEAKAIIVATGKGKHEAGTEGES 119
QY 126 ELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGFTTKFKADKVTIHRDELRAQRI 185
DB 120 AFITGRGVSYCATCDGNFGRKGVIVYSGKEAIEDALYLDIGCEVTIVSRTSFRAEKA 179
QY 186 LQRAFNKDKIDFTWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYGMKPLT 245
DB 180 LVREEVKG-IPVHYSTIRKI-IGSGKVEKVAYNREKKEPEIEADGIFVAIGMRPAT 237
QY 246 APFKDLGITND-VGYIVTKDDMTSVPGIFAAAGDVROKGLRQIVTATGDSIAQAASAEY 304
DB 238 DWAEELGVDSMGYIKVDKEQRTNVEGVFAAGDCDNLKQVVTACDGDGAVAAYSAYKY 297
QY 305 I 305
DB 298 L 298

RESULT 9
US-09-134-000C-3897
; Sequence 3897, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3897
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3897

Query Match          34.4%; Score 571.5; DB 4; Length 329;
Best Local Similarity 39.0%; Pred. No. 8.6e-49;
Matches 120; Conservative 58; Mismatches 123; Indels 7; Gaps 3;

QY 3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPFGFEMITGP 62
DB 238 DWAEELGVDSMGYIKVDKEQRTNVEGVFAAGDCDNLKQVVTACDGDGAVAAYSAYKY 297

; GENERAL INFORMATION:
; APPLICANT: Lanahan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Archaeoglobus fulgidus
US-09-598-747-7

Query Match          34.6%; Score 575; DB 4; Length 300;
Best Local Similarity 43.2%; Pred. No. 3.4e-49;
Matches 130; Conservative 53; Mismatches 112; Indels 6; Gaps 6;

QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPFGFEMITGPDLS 66
DB 2 YDVAIIGGAGLTAALYSARYGLKTVFFETVDPVSLSLAAKIENYVPGFEG-SGMELLE 60
QY 67 KMFEHAKKFGAVYQYGDIKSVDEKGE-YKVINFGNKELTAKAVIIATGAAYKKIGVPEQ 125
DB 61 KMKEQAVKAGAEKWLKVERVNERGETFTVIAEGG-EYEAKAIIVATGKGKHEAGTEGES 119
QY 126 ELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGFTTKFKADKVTIHRDELRAQRI 185
DB 120 AFITGRGVSYCATCDGNFGRKGVIVYSGKEAIEDALYLDIGCEVTIVSRTSFRAEKA 179
QY 186 LQRAFNKDKIDFTWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYGMKPLT 245
DB 180 LVREEVKG-IPVHYSTIRKI-IGSGKVEKVAYNREKKEPEIEADGIFVAIGMRPAT 237
QY 246 APFKDLGITND-VGYIVTKDDMTSVPGIFAAAGDVROKGLRQIVTATGDSIAQAASAEY 304
DB 238 DWAEELGVDSMGYIKVDKEQRTNVEGVFAAGDCDNLKQVVTACDGDGAVAAYSAYKY 297
QY 305 I 305
DB 298 L 298

RESULT 10
US-09-540-014-25
; Sequence 25, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-540-014-25

Query Match          34.3%; Score 569.5; DB 4; Length 321;
Best Local Similarity 42.1%; Pred. No. 1.3e-48;
Matches 136; Conservative 55; Mismatches 115; Indels 17; Gaps 8;

QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPFGF-EMI 59
DB 1 MGTTKHSLILGSGPAGYTAAYARLANLQPVLTGMEKGGQLTTTTEVENWFGDPNDL 60
QY 60 TGPDLSTKMFHAKKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIIATGAAYKKI 119
DB 61 TGPLLMERHEHATKFEIIFDHINKVDLQNRPFRLNGDNGEYTCDAIIATGASARYL 120
QY 120 GVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGFTTKFKADKVTIHRRDE 179
DB 121 GLPSEAPKRGVSCATCDGFFYRNQKVAVIGGNTAVEALYLSNTIASEVHLIHRDDG 180
QY 180 LRAQRILODRAFFKNKID-FIWSHTTKSINEKDKG--VGSVTLTSTKDGSE-ETHEAD 233
DB 181 FRAEKILIKRLM--DKVENGNIILHNTLTLEVTGDMQVTVRLRDTQNSDNIESLDVA 238
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QY 234 GUYFIYGMKPLTAPFK-DLGIITNDVGYIVTKDDM-----TTSPVGIFAAGDVDRDKLCROI 287
Db :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
239 GLFVAIGHSPNTAIFEGOLEN--GYYKVQSIIHGNAQTGIPGVFAAGDVMDSHIYROA 296
QY 288 VTATGDGSIAAQSAAEYIEHLND 310
Db :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
297 ITSAGTCGMAALDAERYLDGLAD 319

RESULT 11
US-09-489-039A-12096
; Sequence 12096, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12096
; LENGTH: 349
; TYPE: PR1
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12096

Query Match 34.2%; Score 568.5; DB 4; Length 349;
Best Local Similarity 40.7%; Pred. No. 1.9e-48;
Matches 136; Conservative 51; Mismatches 114; Indels 33; Gaps 8;

QY 1 MGTEIDFDIAIIGAGPAGMTAAVVASRANLKTYMIERGIPCGQWANTEEVENPPGF-EMI 59
Db :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
28 MGTAKSKLLILGSGPAGYTAAVTAARANLPVLITQMEXGGQLTTTTEVENWPGDPNDL 87
QY 60 TGPDLSITKMEHAKFGAVCYQGDIKSVE-----DKGEYKVINFGNKELTAKAVI 109
Db :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
88 TGPLLMERMEHAAKPETEIFOHSRVDLQNRPRLTGDSGEY-----TCDALI 137
QY 110 IATGAEEYKLGVPGEQELGGRGVSVCACDGAFKKNRFLVFIGGDSABEGFTTKFAD 169
Db :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
138 IATGASARYLGLSEEFEEKRGVSACATCDGFFYRNKGAVIGGNTAVEEALYSNIAS 197
QY 170 KVTVIHRRDELRAQRILQDRAFKNKDIDETWSHTTKSINEKDGK---VGSVTTLSTKDG 226
Db :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
198 EVHLIHRROSFRREKLILKELMDKVASGNIVLTDRILEVTGDMQVSGRLRDTKNSD 257
QY 227 E-ETHRADGVFIYIMKPLTAPFK-DLGITNDVGYIVTKDDM-----TTSVPGIFAAGDV 279
Db :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
258 NVESLEVAGLFVAIGHSPNTAIFEGOLEN--GYIKVQSGIHGNATQISIPGVFAAGDV 315
QY 280 RKGLRQIVTATGDSIAAQSAAEYIEHLNDQAR 313
Db :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
316 MDHIYRQAITSAGTCGMAALDAERYLDGLADACK 349

RESULT 12
US-540-014-24
; Sequence 24, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014

193 RASKIMQARALSNPKIQVMD---SEVVVAYGAGGGPLAGVKVKNLVTGEVSDLOVSGSL 249
236 FYIYGMKPLTAPFKDLGITNDVGYIVTVDKDMT-TSVPGIFAAAGDVRDKGLRQIVTATG 294
250 FPAIGHPEPATKFNQLELHADGYVATKPGSTHTSVGVFAAGDVQDKKYRQAITAAGSG 309
295 SIAQSAABEYIEHLNDQ 311
310 CWAALDAEHLQEVGAQ 326
RESULT 15
US-08-386-729A-7
; Sequence 7, Application US/08386729A
; Patent No. 5753435
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.
; APPLICANT: Schreiber, Rachel
; APPLICANT: Argaman, Anat
; APPLICANT: Av-Gay, Yossef
; APPLICANT: Nan, Helena M.
; APPLICANT: Kattavilder, Alfred
; APPLICANT: Pallisa, Harriet
; TITLE OF INVENTION: An oxido reductase enzyme system
; TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
; TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
; TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
; TITLE OF INVENTION: production
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weil, Gotshal & Manges
; STREET: 2882 Sand Hill Road, Ste. 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,729A
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/274,043
; FILING DATE: 12-JULY-1994
; APPLICATION NUMBER: US 07/820,688
; FILING DATE: 24-MARCH-1992
; APPLICATION NUMBER: PCT/NL91/000101
; FILING DATE: 18-JUNE-1991
; APPLICATION NUMBER: EP 90201598.1
; FILING DATE: 18-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-024/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6200
; TELEFAX: (415) 854-3713
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-386-729A-7

Query Match

30.9%; Score 513.5; DB 1; Length 334;

17 VILIGSGPAGYAAVYARANKPLLIITGMQAGGLTTTTEVDNPNPDPHGHTGALMOR 76
68 MEHAKKFCAVYQYGDIKSVEDKGEYKVFNGKELTAKAVIIATGAEEKIKGVPEQEL 127
77 MQEHAERFETEIVFOHIIHADVLAGKFTURGNGIYTCDALIVATGASARYLGLPSEQAF 136
128 GGRGVSYCAVCDGAFKFNKRLFYIGGDSAVBEGTFTTKFADKVTIVHRRDELRAQRILO 187
137 MKGVSAACATCDGFFVYRNEVAVIGGNTAVEEALYLANIAGRVTLVHRRFTRAEKILQ 196
188 DRAFKNKIDFINSHTTKSINEKDGKGVSVT--LTSTKGSBETHADGVFIYGMKPLT 245
197 DKLQARVAEGKIVLKLNAEVDVLGDMGTGTVRLKTRDGGSEIAVDGMFVAIHTPNT 256
246 APFKDLGITNDVGYIVTK-----DDMTTSPVGFIFAAGDVRDKGLRQIVTATGDSIAAQS 300
257 SLEFGQIALKD-GYLVVNGREGNATATNPGVFAAGDVADHYRQAITAGAGCWAALD 315
301 AAEEYIEHL 308
316 VERYLDL 323
RESULT 14
US-09-540-014-9
; Sequence 9, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresoxin and
; TITLE OF INVENTION: NADP-Thioresoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-540-014-9
Query Match
Best Local Similarity 31.6%; Score 524.5; DB 4; Length 332;
Matches 124; Conservative 44; Mismatches 132; Indels 17; Gaps 6;
9 IAIIGAGPAGTAAVYASRANKVTMIERGI-----PGGOMANTEVENPFGFEM-ITGP 62
13 VCIIGSGPAAHTAAIYAAARALKPVLFEWGMANDIAAGQLTTTDDVENPFGPFGIMGI 72
63 DLSTKMFHAKKFGAVYQYCDIKSVEDKGEYKVFNGKELTAKAVIIATGAEEKIKGV 122
73 DLMNCRAGSVRFGTILSETVEVDSARPPRVTSITVLADTVVATGAVARLHFS 132
123 GQELGGRGVSYCAVCDGA--FPKRLFLVIGGDSAVBEGTFTTKFADKVTIVHRRDEL 180
133 GSDTYNNRGISACAVCDGAAPFRNKPFAVIGGDSAMBEGNFLTKYGSQVLIHRRNTP 192
181 RAQRILQDRAFKNDKIDFIWHTTKSINEXKDGKGVSVTLTSTK-----DGSEETHRADGV 235

Search completed: September 15, 2004, 12:22:10
Job time : 33 secs

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OM protein - protein search, using sw model

Run on:

September 15, 2004, 12:05:48 ; Search time 125 Seconds
(without alignments)
723.322 Million cell updates/sec

Title:

Perfect score: 1662

Sequence: 1 MGTEIFDPIAIIAGPAGMT.....ADYIEHLNDQARPHHHHH 320

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1662	100.0	320	5	ABP04148
2	1593	95.8	312	4	Au00834
3	1582	95.2	311	6	Abm72250
4	1573	94.6	309	6	Ada89500
5	1561	93.9	311	2	AAY29854
6	1561	93.9	311	5	ABP0916
7	1455	87.5	310	2	RAY29855
8	1455	87.5	310	4	AA82024
9	1154	69.4	315	5	ABP60849
10	1154	69.4	315	6	AAO20618
11	1152	69.3	315	6	AD26553
12	1145.5	68.9	315	5	ABP60886
13	1090	65.6	309	7	ADD26570
14	1083	65.2	319	5	ABP40667
15	1054	63.4	319	5	ABP60863
16	1054	63.4	319	5	ABP60904
17	929.5	55.9	324	6	ABD08826
18	899	54.1	305	5	ABP26879
19	872	52.5	308	5	ABP54256
20	872	52.5	308	5	ABP60904
21	852.5	51.3	304	5	ABP26878
22	849	51.1	303	5	ABP60919
23	849	51.1	303	6	ABU01907
24	849	51.1	303	6	ABU01907
25	753	45.3	314	5	ABP60894

26	728.5	43.8	325	5	ABP60895
27	726	43.7	315	5	ABP60859
28	706	42.5	315	5	ABP60856
29	697.5	42.0	307	5	ABP60875
30	687	41.3	317	5	ABP60930
31	647.5	39.0	341	5	ABP65642
32	645.5	38.8	345	4	ABP65642
33	645.5	38.8	345	5	ABP60914
34	644.5	38.8	321	5	ABP60873
35	639.5	38.5	335	5	ABP60868
36	635.5	38.2	354	6	ABM65731
37	632.5	38.1	458	5	ABP60865
38	632.5	38.1	458	5	ABP60778
39	632.5	38.1	458	5	ABP60694
40	632.5	38.1	458	5	ABP60702
41	632.5	38.1	458	6	AAO20628
42	632.5	38.1	458	6	AAO20619
43	632.5	38.1	458	7	ADD26554
44	632.5	38.1	513	5	ABP60691
45	629.5	37.9	326	5	ABP60917

ALIGNMENTS

RESULT 1

ID ABB04148 standard; protein; 320 AA.

XX ABB04148;

AC

DT 20-MAR-2002 (first entry)

XX

DE Recombinant Staphylococcus aureus thioredoxin reductase (TrxB).

XX

KW Thioredoxin reductase; molecular complex; crystal; inhibitor;

KW Three dimensional structure; flavin adenine dinucleotide; reduced;

KW protein co-ordinate data; TrxB; FAD; NADPH; rational drug design;

KW 3D structure; beta-nicotinamide adenine dinucleotide phosphate.

XX

OS Staphylococcus aureus.

OS Synthetic.

XX

FT Key

FT Binding-site

FT Binding-site

FT Binding-site

FT Binding-site

FT Binding-site

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FT Binding-site

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FT Binding-site

WO200177309-A2.
18-OCT-2001.
03-APR-2001; 2001WO-US010678.
06-APR-2000; 2000US-0195055P.
(PHAA) PHARMACIA & UPOJOHN CO.
Benson TE;
MPI; 2002-034237/04.
Crystallising Staphylococcus aureus thioredoxin reductase molecule or molecular complex by preparing purified thioredoxin reductase and crystallizing from solution comprising dimethyl sulfoxide and sodium formate.
Claim 52; Fig 11; 147pp; English.
The present sequence is that of a recombinant Staphylococcus aureus thioredoxin reductase ("rxB") the crystal structure of which is solved in the specification. Thioredoxin reductase is a two domain protein composed of a flavin adenine dinucleotide (FAD) binding domain and a reduced beta-nicotinamide adenine dinucleotide phosphate (NADPH) binding domain. The specification describes the crystallisation of S. aureus thioredoxin reductase molecule or molecular complex. The crystal of the invention may be used to design an inhibitor of S. aureus thioredoxin reductase activity. The method is useful for crystallising a S. aureus thioredoxin reductase molecule or molecular complex. The crystal obtained is useful for solving the structure of other molecules or molecular complexes and designing inhibitors of S. aureus thioredoxin reductase. A composition comprising the inhibitor is useful for preventing and treating S. aureus thioredoxin reductase mediated disease

XX	Sequence 320 AA;
SQ	
	Query Match 100.0%; Score 1662; DB 5; Length 320; Best Local Similarity 100.0%; Pred. No. 3e-146; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MGTEIDFDIATGAGPAGMTAAVYAGRANLKTVMIERIGPGQMANTEEVENPPGFEMIT 60 Db 1 MGTEIDFDIATGAGPAGMTAAVYAGRANLKTVMIERIGPGQMANTEEVENPPGFEMIT 60
QY	61 GPDLSTKMFHAHKKFGAVQYGDIKSVEDKGEYKVINFNGKELTAKAVIIATGAEYKKIG 120 Db 61 GPDLSTKMFHAHKKFGAVQYGDIKSVEDKGEYKVINFNGKELTAKAVIIATGAEYKKIG 120
QY	121 VPQEQLGGRGVS YCAVCDGAFKNKRLFVIGGDSAVEEGTFTTKEADKVTIVHRRDEL 180 Db 121 VPQEQLGGRGVS YCAVCDGAFKNKRLFVIGGDSAVEEGTFTTKEADKVTIVHRRDEL 180
QY	181 RAQRILLQDRAFKNDKIDFIWSHTTKSINERDKGVSVTLTSTKDGSSETHADGVFIYIG 240 Db 181 RAQRILLQDRAFKNDKIDFIWSHTTKSINERDKGVSVTLTSTKDGSSETHADGVFIYIG 240
QY	241 MKPLTAPFKOLGITNDVGYYITVKDDMTTSVPGIFAAGDVDRDKGRQIVTATGDGSIQAQS 300 Db 241 MKPLTAPFKOLGITNDVGYYITVKDDMTTSVPGIFAAGDVDRDKGRQIVTATGDGSIQAQS 300
QY	301 AAEYIEHLNQARSHHHHH 320 Db 301 AAEYIEHLNQARSHHHHH 320
RESULT 2	
AAU00834	
ID	AAU00834 standard; protein; 312 AA.
XX	
AC	AAU00834;
XX	
DT	04-JUL-2001 (first entry)
XX	
DE	S. aureus thioredoxin reductase, TrxB.
XX	
KW	Thioredoxin reductase; TrxB; immunogen; vaccine; antibody;
KW	wound infection; cellulitis; burn infection; eyelid infection;
KW	food poisoning; joint infection; neonatal conjunctivitis; osteomyelitis;
KW	skin infection; scalded skin syndrome; toxic epidermal necrosis;
KW	Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis.
OS	Staphylococcus aureus.
XX	
FH	Key Location/Qualifiers
FT	Region 192..194
FT	/label= Antigenic_epitope
FT	Region 210..212
FT	/label= Antigenic_epitope
XX	
PN	WO200116292-A2.
XX	
PD	08-MAR-2001.
XX	
PP	31-AUG-2000; 2000WO-US023773.
XX	
PR	01-SEP-1999; 99US-0151933P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Choi GH;
XX	
DR	WPI; 2001-183259/18.
XX	
N-PSDB; AAS00915.	
XX	
PT	New isolated nucleic acid for use in diagnosing Staphylococcus infections.
XX	
PT	and in vaccines for eliciting immune responses to the infections.

XX PS Claim 9; Page 16; 225pp; English.

XX CC The sequence represents *S. aureus* TrxB (Thioredoxin reductase). The

XX CC polynucleotides of the invention are used to detect *Staphylococcus*

XX CC nucleic acids in a biological sample from an animal for diagnosing

XX CC *Staphylococcus* infections. The polypeptides of the invention are used to

XX CC detect anti-*Staphylococcus* antibodies in a biological sample from an

XX CC animal to diagnose *Staphylococcus* infections. The polypeptides are also

XX CC used in vaccines to elicit protective antibodies in an animal to a member

XX CC of the *Staphylococcus* genus and for preventing or attenuating an

XX CC infection caused by a member of the *Staphylococcus* genus e.g. wound

XX CC infection, cellulitis, burn infection, eyelid infection, food poisoning,

XX CC joint infection, neonatal conjunctivitis, osteomyelitis, skin infection,

XX CC scalded skin syndrome (also known as toxic epidermal necrosis, Ritter's

XX CC disease and Lyell's disease), toxic shock syndrome and endocarditis. The

XX CC polynucleotides may also be used in vaccines and for preventing or

XX CC attenuating a *Staphylococcus* infection. Antibodies to the polypeptides

XX CC may be used to purify, detect and target the polypeptides in vitro and

XX CC in vivo diagnostic and therapeutic methods

XX SQ Sequence 312 AA;

Query Match 95.8%; Score 1593; DB 4; Length 312;
Best Local Similarity 99.4%; Pred. No. 7.7e-140;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANKLTVMIERGIPGGQMANTEEVNPPGEMIT 60
Db |||||
QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANKLTVMIERGIPGGQMANTEEVNPPGEMIT 60
Db |||||

QY 61 GPDLSKTFEHAHKKFAGVYQYGDIKSVDEKGEYKVINFGNKLTAKAVIATGAEYKKG 120
Db |||||

QY 61 GPDLSKTFEHAHKKFAGVYQYGDIKSVDEKGEYKVINFGNKLTAKAVIATGAEYKKG 120
Db |||||

QY 121 VPGEQLGGRGVSVCVCDGAFKFKRLFVIGGDSAVEEGTFTKPADKVTIVHRRDEL 180
Db |||||

QY 121 VPGEQLGGRGVSVCVCDGAFKFKRLFVIGGDSAVEEGTFTKPADKVTIVHRRDEL 180
Db |||||

QY 181 RAQRILQDRAFKNDKIDFIWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIG 240
Db |||||

QY 181 RAQRILQDRAFKNDKIDFIWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIG 240
Db |||||

QY 241 MKPLTAPFKDLGITNDVGVIYTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQS 300
Db |||||

QY 241 MKPLTAPFKDLGITNDVGVIYTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQS 300
Db |||||

QY 301 AAIEYIEHLNDQA 312
Db |||||

QY 301 AAIEYIEHLNDQA 312
Db |||||

RESULT 3
BM72250
ID BM72250 standard; protein; 311 AA.
XX AC
XX BM72250;
XX
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus protein #1490.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.
XX
XX Staphylococcus aureus.
XX
XX WC200294868-A2.
XX
XX 28-NOV-2002.
XX
XX 27-MAR-2002; 2002NO-IB002637.
XX

PR 27-MAR-2001; 2001GB-00007661.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Masignani V, Mora M, Scarselli M;
XX
XX WPI: 2003-120786/11.
XX N-PSDB; ACF73810.
XX
XX New *Staphylococcus aureus* protein, useful as a vaccine for treating or
XX preventing *Staphylococcus* infection, specifically an infection caused by
XX *S. aureus*, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 2980; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
XX *Staphylococcus aureus*. A composition comprising the *S. aureus* protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to *Staphylococcus* bacteria, specifically an
XX infection caused by *S. aureus*. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel *S. aureus* proteins of the invention
XX
XX SQ Sequence 311 AA;

Query Match 95.2%; Score 1582; DB 6; Length 311;
Best Local Similarity 99.4%; Pred. No. 8.1e-139;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TEIDFDIAIIGAGPAGMTAAVYASRANKLTVMIERGIPGGQMANTEEVNPPGEMITGP 62
Db |||||

QY 2 TEIDFDIAIIGAGPAGMTAAVYASRANKLTVMIERGIPGGQMANTEEVNPPGEMITGP 61
Db |||||

QY 63 DLSTKMFHAKFAGVYQYGDIKSVDEKGEYKVINFGNKLTAKAVIATGAEYKKG 122
Db |||||

QY 62 DLSTKMFHAKFAGVYQYGDIKSVDEKGEYKVINFGNKLTAKAVIATGAEYKKG 121
Db |||||

QY 123 GEQELGGRGVSVCVCDGAFKFKRLFVIGGDSAVEEGTFTKPADKVTIVHRRDELRA 182
Db |||||

QY 122 GEQELGGRGVSVCVCDGAFKFKRLFVIGGDSAVEEGTFTKPADKVTIVHRRDELRA 181
Db |||||

QY 183 QRILQDRAFKNDKIDFIWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIG 242
Db |||||

QY 182 QRILQDRAFKNDKIDFIWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIG 241
Db |||||

QY 243 PLTAPFKDLGITNDVGVIYTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQSAA 302
Db |||||

QY 242 PLTAPFKDLGITNDVGVIYTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQSAA 301
Db |||||

QY 303 EYIEHLNDQA 312
Db |||||

QY 302 EYIEHLNDQA 311
Db |||||

RESULT 4
ADA89500
ID ADA89500 standard; protein; 309 AA.
XX
XX ADA89500;
XX
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus antigenic protein #39.
XX
XX antigenic protein; vaccine; *Staphylococcus aureus*; pathogenic organism;
XX antibacterial; neuroprotective; immunosuppressive; antiinflammatory;
XX antiulcer; immunostimulant; ophthalmological; pathogenic microbe;
XX bacteraemia; septic shock; organ infection; skin infection;
XX bacterial basal colonisation; bacterial eye infection; septicemia;
XX tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;

sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
 necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
 gastro-enteritis; dysentery; shigellosis; skin disorder.
 Staphylococcus aureus.
 WO2003011899-A2.
 13-FEB-2003.
 02-AUG-2002; 2002WO-CB003606.
 02-AUG-2001; 2001GB-00018825.
 09-JAN-2002; 2002GB-00000349.
 (UYSH-) UNIV SHEFFIELD.
 (BIOS-) BIOSYNEXUS INC.
 Foster S, Mond J, Clarke S, McDowell P, Brummel K;
 WPI; 2003-256434/25.
 New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
 useful as a vaccine for immunizing humans against e.g. bacteremia, septic
 shock, septicaemia, tuberculosis, meningitis, pneumonia, gonorrhoea or
 impetigo.
 Claim 4; Page 131; 189pp; English.
 The present invention describes an antigenic protein or its part, which
 is for use as a vaccine. The antigenic protein is encoded by an isolated
 DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
 sequences (designated dnaA and dna SE, respectively; and which encodes a
 protein expressed by a pathogenic organism. Also described: (1) a vaccine
 composition comprising at least one antigenic protein; (2) a method of
 immunising an animal against a disease or condition caused by a
 pathogenic microbe by administering the antigenic protein or the vaccine;
 (3) an antibody or its binding part obtainable by the method above; (4)
 preparing a hybridoma cell line producing monoclonal antibodies; (5) a
 hybridoma cell line produced by the method of (4); and (6) identifying
 opsonic antigens expressed by a pathogenic microbe. The antigenic
 proteins have antibacterial, neuroprotective, immunosuppressive,
 antiinflammatory, antitumor, immunostimulant and ophthalmological
 activities, and can be used in vaccines. The antigenic proteins or
 vaccines can be used for immunising an animal (specifically a human)
 against a disease or condition caused by a pathogenic microbe, e.g.
 bacteremia, septic shock, organ infection, skin infection, bacterial
 basal colonisation, bacterial eye infections, septicemia, tuberculosis,
 bacteria-associated food poisoning, blood infections, peritonitis,
 endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
 strep throat, streptococcal-associated toxic shock, necrotising
 fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
 dysentery, shigellosis, S. aureus-associated septicemia, food poisoning,
 skin disorders, S. epidermidis-associated septicemia, peritonitis or
 endocarditis. The present sequence represents a S. aureus antigenic
 protein sequence from the present invention.
 Query Match 94.6%; Score 1573; DB 6; Length 309;
 Best Local Similarity 99.4%; Pred. No. 5.6e-138;
 Matches 306; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 3 TEIDFDIAIIGAGPAGMTAAVYASRANKTVMIERGIPGGQMANTEVEENFFGEMITGP 62
 2 TEIDFDIAIIGAGPAGMTAAVYASRANKTVMIERGIPGGQMANTEVEENFFGEMITGP 61
 63 DLSTKMFHAKFGAVYQYGDVKSVDKGEYKVFNGKELTAKAVIIATGAEYKKGIVP 122
 62 DLSTKMFHAKFGAVYQYGDVKSVDKGEYKVFNGKELTAKAVIIATGAEYKKGIVP 121
 123 GEOLGGRGVSYCAVCDGAPFKNKRLFVIGGDSAVEEGTFTTKADKVTIIVHRRDELRA 182

Db 122 GEOLGGRGVSYCAVCDGAPFKNKRLFVIGGDSAVEEGTFTTKADKVTIIVHRRDELRA 181
 QY 183 QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
 Db 182 QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 241
 QY 243 PLTAPFCKDLGTTNDVGYIVTKDDMTTSVPGIFAGDVRDKGLRQIVTATGDSIAAQAASAA 302
 Db 242 PLTAPFCKDLGTTNDVGYIVTKDDMTTSVPGIFAGDVRDKGLRQIVTATGDSIAAQAASAA 301
 QY 303 EYIEHLND 310
 Db 302 EYIEHLND 309
 RESULT 5
 AAY29854
 ID AAY29854 standard; protein; 311 AA.
 AC
 XX AAY29854;
 DT 17-NOV-1999 (first entry)
 XX
 XX Staphylococcus aureus trx8 open reading frame protein sequence.
 DE
 XX Staphylococcus; trx8; thioredoxin reductase; antimicrobial.
 KW
 XX Staphylococcus aureus.
 OS
 XX WO9945123-A1.
 PN
 XX 10-SEP-1999.
 PD
 XX 02-MAR-1999; 99WO-US004512.
 PF
 XX 02-MAR-1998; 98US-0076525P.
 PR
 XX (ABBO) ABBOTT LAB.
 PA
 XX Aharonowitz Y, Borovok I, Cohen G, Uziel O, Katz L;
 PI
 XX WPI; 1999-551044/46.
 XX
 XX N-PSDB; AAZ21080.
 XX
 XX A new thioredoxin reductase from Staphylococcus aureus.
 PT
 XX Claim 2; Fig 2; 59pp; English.
 PS
 XX The present sequence represents Staphylococcus thioredoxin reductase
 CC (TrxB). TrxB inhibitors can be used as antimicrobials to treat a
 CC Staphylococcus, particularly S. aureus, infection. TrxB inhibitors are
 CC antimicrobials to which, unlike most of those in the prior art,
 CC Staphylococcus has not yet developed a resistance
 XX
 SQ Sequence 311 AA;
 Query Match 93.9%; Score 1561; DB 2; Length 311;
 Best Local Similarity 98.1%; Pred. No. 7.4e-137;
 Matches 304; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 3 TEIDFDIAIIGAGPAGMTAAVYASRANKTVMIERGIPGGQMANTEVEENFFGEMITGP 62
 2 TEIDFDIAIIGAGPAGMTAAVYASRANKTVMIERGIPGGQMANTEVEENFFGEMITGP 61
 63 DLSTKMFHAKFGAVYQYGDVKSVDKGEYKVFNGKELTAKAVIIATGAEYKKGIVP 122
 62 DLSTKMFHAKFGAVYQYGDVKSVDKGEYKVFNGKELTAKAVIIATGAEYKKGIVP 121
 123 GEOLGGRGVSYCAVCDGAPFKNKRLFVIGGDSAVEEGTFTTKADKVTIIVHRRDELRA 182
 122 GEOLGGRGVSYCAVCDGAPFKNKRLFVIGGDSAVEEGTFTTKADKVTIIVHRRDELRA 181
 QY 183 QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242

Db 182 QRILQDRAFKNDKIDFIWSHTLKSINERKDGKVGSVTLSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQSA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQSTS 301
 Qy 303 EYIEHLNDQA 312
 Db 302 GYIEHLNDQA 311

RESULT 6

ABP60916
 ID ABP60916 standard; protein; 311 AA.

XX AC
 XX XX
 XX XX

DT 06-SEP-2002 (first entry)
 XX

DE Staphylococcus aureus thioredoxin reductase SEQ ID NO:265.
 XX

KW Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 KW vasotropic; vulnery; antibacterial; immunosuppressive; antiulcer;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease.

XX Staphylococcus aureus.
 OS

XX WO200250289-A1.
 PN

XX 27-JUN-2002.
 PD

XX 19-DEC-2001; 2001WO-US050240.
 PF

XX 19-DEC-2000; 2000US-00742900.
 PR

XX 05-JUL-2001; 2001US-0302885P.
 PR

XX 04-DEC-2001; 2001US-00006038.
 PR

PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA

XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX

PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX

DR WPI; 2002-508806/54.
 DR

XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.

XX Claim 82; Page 315-316; 362pp; English.
 XX

CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD); cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease (COPD); cataracts,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD

CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 311 AA;

Query Match 93.9%; Score 1561; DB 5; Length 311;
 Best Local Similarity 98.1%; Pred. No. 7.4e-137;
 Matches 304; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEVPPGFEMITGP 62
 Db 2 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVEVPPGFEMITGP 61
 Qy 63 DLSTKMEFAHAKTGAIVYQYGDIIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKIGVP 122
 Db 62 DLSTKMEFAHAKTGAIVYQYGDIIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKIGVP 121
 Qy 123 GEQELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
 Db 122 GEQELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA 181
 Qy 183 QRILQDRAFKNDKIDFIWSHTLKSINERKDGKVGSVTLSTKDGSEETHEADGVFIYIGMK 242
 Db 182 QRILQDRAFKNDKIDFIWSHTLKSINERKDGKVGSVTLSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQSA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSIAAQSTS 301
 Qy 303 EYIEHLNDQA 312
 Db 302 GYIEHLNDQA 311

RESULT 7

AAV29855
 ID AAV29855 standard; protein; 310 AA.

XX AC
 XX AAV29855;

XX DT 17-NOV-1999 (first entry)
 XX

DE Staphylococcus epidermidis trxB open reading frame protein sequence.
 XX

KW Staphylococcus; trxB; thioredoxin reductase; antimicrobial.
 XX

OS Staphylococcus epidermidis.
 XX

XX WO9945123-A1.
 PN

XX PD 10-SEP-1999.
 PD

XX PF 02-MAR-1999; 99WO-US004512.
 PF

XX PR 02-MAR-1998; 98US-0076525P.
 PR

XX PA (ABBO) ABBOTT LAB.
 PA

XX PI Aharonowitz Y, Borovok I, Cohen G, Uziel O, Katz L;
 PI

XX DR WPI; 1999-551044/46.
 DR

XX DR N-PSDB; AAZ221081.
 DR

XX A new thioredoxin reductase from Staphylococcus aureus.
 XX

XX Claim 2; Fig 7; 59pp; English.
 XX

CC The present sequence represents Staphylococcus thioredoxin reductase
 CC (TrxB). TrxB inhibitors can be used as antimicrobials to treat a
 CC Staphylococcus, particularly S. aureus, infection. TrxB inhibitors are
 CC antimicrobials to which, unlike most of those in the prior art,
 CC Staphylococcus has not yet developed a resistance

[illegible]

123	GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA	182
QY		
122	GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRA	181
Db		
183	QRILQBRAFKNDKIDFTWSHTTKSINEKDGKGVSVTLTSTKDGSEETHADGVFIYIGMK	242
QY		
182	QNILQBRAFKNDKVDFITWSHTTKTINEKDGKGVSVTLTSTKDGAEQTYDADGVFIYIGMK	241
Db		
243	PLTAPPKDLGITNDVGIVYTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSA	302
QY		
242	PLTAPPKNLGITNDAGYIVTQDDMSTKVRGIFAAGDVRDKGLRQIVTATGDGSIAAQSA	301
Db		
303	EYIEHLND	310
QY		
302	DYITELKD	309
Db		

[illegible]

Db	182	QNTLQRAFRKNDKVDFTWSHTLKTINEKDGKVGSVTLSETKDGAETQYDADCVFIYIGMK	241
QY	243	PLTAPFKDLGITNDVGVIVTKDDMTTSVPGIFAAQGDVRDKGLRQIVATGSGTAAQAA	302
Db	242	PLTAPFKNLGITNDAGYIVTQDDMTSKVGRGIFAAQGDVRDKGLRQIVATGSGTAAQAA	301
QY	303	EYIEHLND 310	
Db	302	DYITELKD 309	

[illegible]

QY 303 EYIEHLND 310
: || |
Db 302 DYITELKD 309

AAG82024
ID AAG82024 standard; protein; 310 AA.

AC AAG82024;
XX
XX
02 APR 2004 (filed entry)

XX
DE
v
S. epidermidis open reading frame protein sequence SEQ ID NO:1142.

KW Staphylococcus epidermidis SK1 strain; infection; diagnosis; treatment
 KW endocarditis.
 XX
 XX

US staphylococcus epidermidis.
XX
PN WO200134809-A2.

17-MAY-2001.

XX
PR 09-NOV-1999; 99US-0164258P.

PA (GLAX) GLAXO GROUP LTD.
XX
XX
XX

XX
DR WPI; 2001-316495/33.
N. 8078. AAU52874

XX
PT
Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
useful for vaccinating against infections, e.g. endocarditis.

XX
PS
Claim 18; Page 330; 2188pp; English.
XX

(II) and (II) can have antibacterial activity and therefore can be used in

epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the

[illegible]

RESULT 11	
ADD26553	
ID	ADD26553 standard; protein; 315 AA.
XX	
AC	ADD26553;
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	B. subtilis thioredoxin reductase.
XX	
KW	Thioredoxin reductase; TRR; cofactor specificity;
KW	computational mutagenesis; substrate specificity; PDA;
KW	protein design automation; toxic protein; food allergenicity;
KW	food digestibility.
XX	
OS	Bacillus subtilis.
XX	
PN	US2003100743-A1.
XX	
PD	29-MAY-2003.
XX	
PF	06-MAY-2002; 2002US-00141531.
XX	
PR	04-MAY-2001; 2001US-0289029P.
PR	03-APR-2002; 2002US-0370609P.
PR	29-APR-2002; 2002US-0376682P.
XX	
PA	(DALM/) DALMIA B K.
PA	(BRIG/) BRIGGS S P.
PA	(VALG/) VAL G D.
PA	(DESJ/) DESJARLAIS J R.
PA	(HEIF/) HEIFETZ P.
PA	(LUGI/) LUGINBUHL P.
PA	(MUCH/) MUCHHAL U.
XX	
PI	Dalmia BK, Briggs SP, Val GD, Desjarlais JR, Heifetz P;
PI	Luginbuhl P, Muchhal U;
XX	
DR	WPI; 2003-801212/75.

PT Altering the cofactor specificity of thioredoxin reductase, useful for
PT reducing the toxicity of toxic proteins, reducing allergenicity of food
PT and increasing the digestibility of foods, comprises computational
PT mutagenesis.

XX Disclosure; Fig 21; 125pp; English.

XX The invention relates to altering the cofactor specificity of thioredoxin
XX reductase (TRR) comprising computational mutagenesis. Also included are
CC altering the substrate specificity of TRR or cofactor specificity of a
CC target protein, a variant TRR protein that reduces a protein that reduces
CC a thioredoxin protein (obtained from an organism selected from
CC *Escherichia coli*, *Bacillus subtilis*, *Mycobacterium leprae*, *Saccharomyces*,
CC *Neurospora crassa*, *Arabidopsis*, and human), a variant TRR protein fused
CC to a second protein (that is either a wild-type TRR protein, thioredoxin,
CC or a variant TRR protein), producing a plant with a modified TRR protein,
CC a transformed plant prepared by the method and a transformed seed of the
CC transformed plant. The cofactor specificity of the variant TRR is altered
CC such that the variant preferentially binds NADPH compared to NADH, or
CC vice versa. The protein design cycle comprises the sequence design automation
CC (FDA (RTM)). This design cycle comprises the sequence design algorithm,
CC or a force field calculation. The variant TRR protein is fused to the
CC second protein through a linker. The variant TRR protein has 1-3 amino
CC acid substitutions as compared to the wild-type Arabidopsis TR protein.
CC The amino acid substitutions are selected from positions A4, A5 and A6,
CC preferably from RA4W, RA5L, RA5M, RA5I, RA5F, RA5Y, RA68, RA68,
CC RA6Q, RA6G, and RA6N. The method is useful for reducing the toxicity of
CC toxic proteins, reducing allergenicity of food and increasing the
CC digestibility of food. The invention provides an efficient and low cost
CC method as compared to prior art. The present sequence is a wild-type TRR
CC protein.

Query Match	69.4%;	Score	1154;	DB	7;	Length	315;
Best Local Similarity	71.4%;	Pred.	No. 6.5e-99;				
MATCHES	220;	Conservative	33;	Mismatches	55;	Indels	0;
Gaps							
QY	7	FDIATIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFFGFEMITGPDILST	66				
Db	6	YDVIIIGAGPAGMTAAVTSTRANLSLTMIERGIPGGQMANTEDVENYPGFESIILGPPELSN	65				
QY	67	KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGCEQE	126				
Db	66	KMFEHAKKFGABAYAGDIKEVIDGKEYKVWRAGSKEYKARAVIIAAGA EYKKIGVPGKE	125				
QY	127	LGRGVSYCAVCDGAFKFNKL FVI GGGDSAVEEGCTFTTKPADKVTIVRRDELRAQRIL	186				
Db	126	LGRGVSYCAVCDGAFKGLVLVVGGGDSAVEEGVYLTRFASKVTIVRRDKLRAQSIL	185				
QY	187	QRAFKNKDIFIWSHTTTSINEKDGKVGSVTLTSTDGSEETHADGVFIYIGMKPLTA	246				
Db	186	QARA PDNEKVDLWNTKYKEIHENGKVGNVTLVDVTGEESEPKTDGVFIYIGMLPLSK	245				
QY	247	PFKDLGITNDVGYIVTKDDMTTSVPDGI PAAGDVDRKGLRQIVTATGDSIAAQSAAEYIE	306				
Db	246	PFENLGITNEEGYIETNDRMETKVGEIFAAGDIRERSLRQIVTATGDSIAAQSVQH YVE	305				
QY	307	HLNQARS	314				
Db	306	ELQETLKT	313				
RESULT 12							
AAO20627							
ID	AAO20627	standard; protein; 315 AA.					
XX	AAO20627						
XX							
XX							
XX							
DE	10-APR-2003	(first entry)					
		Thioredoxin reductase variant protein sequence #26.					

XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occluding body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 XX Sequence 315 AA;

Query Match 68.9%; Score 1145.5; DB 5; Length 315;
 Best Local Similarity 68.6%; Pred. No. 4.1e-98;
 Matches 216; Conservative 38; Mismatches 60; Indels 1; Gaps 1;
 QY 1 MGTEID-FDIAIIGAGPAGMTAAVYASRANKVTVMERIGIPGGOMANTEVENPFGPEMI 59
 DB 1 MGEQKVVYVVIAGAGPAGMTAAVYTSRANLSTVMERIGIPGGOMANTEVENPFGPDHI 60
 QY 60 TGDLSLTKMEHAKKFGAVYQYGDIKSVDEKGVKVFNGKELTAKAVIATGAAYKKI 119
 DB 61 LGPELSTLTKMEHAKKFGAEYAYGDIKEIIDQDGLVKAGNKEVKARAVIATGAAYKKL 120
 QY 120 GVPEQELGGRGVSYCAVCDGAFKKNKRLFVIGGDSAVBEETPTTKFADKVTIVHRDE 179
 DB 121 GVPEKELSGRVSYCAVCDGAFKRELVVVGSDSAVEAVYLTFRASKVTIHRDQ 180
 QY 180 LRAQRILODRAFKNDKIDFINSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIYI 239
 DB 181 LRAQKILQRAFDNDKIEFIWDHVVKQINGTDGKVSSTIEHAKTGQDFKTDGVFIYI 240
 QY 240 GMKPLTAPFKDLGINTDVGIVTDXDMMTTSVPGIPAGDVRDKGLRQIVTATGDSIAAQ 299
 DB 241 GMLPINEAVKLNILNDEGIYVTNEEMETSVPGIPAGDVRDKGLRQIVTATGDSIAAQ 300
 QY 300 SAAEYIEHLNDOARS 314
 DB 301 NVQHYBELAEKVKN 315

RESULT 14
 ADD26570 standard; protein; 309 AA.
 XX ID ADD26570 standard; protein; 309 AA.
 XX AC ADD26570;
 XX DT 15-JAN-2004 (first entry)
 XX DE B. subtilis synthetic thioredoxin reductase.
 XX KW Thioredoxin reductase; TRR; cofactor specificity;
 KW computational mutagenesis; substrate specificity; PDA;
 KW protein design automation; toxic protein; food allergenicity;
 KW food digestibility; mutant; muten.
 XX OS Synthetic.
 XX OS Bacillus subtilis.
 XX OS
 XX PN US2003100743-A1.
 XX PD 29-MAY-2003.
 XX

PF 06-MAY-2002; 2002US-00141531.
 XX
 PR 04-MAY-2001; 2001US-0289029P.
 PR 05-APR-2002; 2002US-0370609P.
 PR 29-APR-2002; 2002US-0376682P.
 XX
 PA (DALM/) DALMIA B K.
 PA (BRIG/) BRIGGS S P.
 PA (VALG/) VAL G D.
 PA (DESI/) DESJARLAIS J R.
 PA (HEIF/) HEIFETZ P.
 PA (LUGI/) LUGINBUHL P.
 PA (MUCH/) MUCHHAL U.
 XX
 PI Dalmia BK, Briggs SP, Val GD, Desjarlais JR, Heifetz P;
 PI Luginbuhl P, Muchhal U;
 XX MPI; 2003-801212/75.
 XX
 PT Altering the cofactor specificity of thioredoxin reductase, useful for
 PT reducing the toxicity of toxic proteins, reducing allergenicity of food
 PT and increasing the digestibility of foods, comprises computational
 PT mutagenesis.
 XX
 PS Claim 30; Page; 125pp; English.
 XX
 CC The invention relates to altering the cofactor specificity of thioredoxin
 CC reductase (TRR) comprising computational mutagenesis. Also included are
 CC altering the substrate specificity of TRR or cofactor specificity of a
 CC target protein, a variant TRR protein that reduces a protein that reduces
 CC a thioredoxin protein (obtained from an organism selected from
 CC Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces,
 CC Neurospora crassa, Arabidopsis, and human), a variant TRR protein fused
 CC to a second protein (that is either a wild-type TRR protein, thioredoxin,
 CC or a variant TRR protein), producing a plant with a modified TRR protein,
 CC a transformed plant prepared by the method and a transformed seed of the
 CC transformed plant. The cofactor specificity of the variant TRR is altered
 CC such that the variant preferentially binds NADPH compared to NADH, or
 CC vice versa. The protein design cycle comprises protein design automation
 CC (PDA (RTM)). This design cycle comprises the sequence design algorithm,
 CC or a force field calculation. The variant TRR protein is fused to the
 CC second protein through a linker. The variant TRR protein has 1-3 amino
 CC acid substitutions as compared to the wild-type Arabidopsis TR protein.
 CC The amino acid substitutions are selected from positions A4, A5 and A6,
 CC preferably from RA4W, RA5L, RA5M, RA5I, RA5F, RA5V, RA5Y, RA6F, RA6S,
 CC RA6Q, RA6G, and RAGN. The method is useful for reducing the toxicity of
 CC toxic proteins, reducing allergenicity of food and increasing the
 CC digestibility of food. The invention provides an efficient and low cost
 CC method as compared to prior art. The present sequence is a synthetic
 CC thioredoxin reductase comprising ligated functional fragments of a wild-
 XX type TRR protein.
 XX Sequence 309 AA;

Query Match 65.6%; Score 1090; DB 7; Length 309;
 Best Local Similarity 69.5%; Pred. No. 5.9e-93;
 Matches 214; Conservative 33; Mismatches 55; Indels 6; Gaps 3;
 QY 7 FDIAIIGAGPAGMTAAVYASRANKVTVMERIGIPGGOMANTEVENPFGPEMIIGPDIST 66
 DB 6 YDVIIIGAGPAGMTAAVYTSRANLSTLMERIGIPGGOMANTEVENPFGPESILGPESLN 65
 QY 67 KMFEHAKKFGAVYQYGDIKSVDEKGVKVFNGKELTAKAVIATGAAYKKIIGVPGQBE 126
 DB 66 KMFEHAKKFGAEYAYGDIKEVIDGKEYKVKWAGSKYKARAVIIAAGAEYKKIIGVPGKE 125
 QY 127 LGGRGVSYCAVCDGAFKKNKRLFVIGGDSAVBEETPTTKFADKVTIVHRDELRAQRI 186
 DB 126 LGGRGVSYCAVCDGAFKRELVVVGSD--VEEGVILTRFASKVTIV---DKL-AQSIL 179
 QY 187 ODRAFKNDKIDFINSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
 DB 180 QARAFDNEKVDFLNKTKVKEIHEENGKVGNTLVDTVTGSESEFKTDGTVFIYIGMLPLSK 239

187 QDRAFNKIDFIWSHTTKSI NEKGKGVSTLTSTXDGSEETHEADGVFIYIGMKPLTA 246

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:13:58 ; Search time 40 Seconds
(without alignments)
769.532 Million cell updates/sec

Title: US-09-825-212-1
Perfect score: 1662
Sequence: 1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1562	95.2	311	2 E89849	thioredoxine reduct
2	1157	69.6	316	1 A69727	thioredoxin-disulf
3	1145.5	68.9	315	2 C84096	thioredoxin reduct
4	1057	63.6	319	2 AH7759	thioredoxin reduct
5	1054	63.4	319	2 APT384	thioredoxin reduct
6	872	52.5	308	2 D86742	thioredoxin-disulf
7	851	51.2	303	2 G98035	thioredoxin-disulf
8	849	51.1	303	2 G95169	thioredoxin reduct
9	728.5	43.8	325	2 A75330	thioredoxin reduct
10	726	43.7	315	1 D35156	thioredoxin-disulf
11	706	42.5	315	1 S63990	thioredoxin-disulf
12	697.5	42.0	307	2 C71278	thioredoxin reduct
13	687	41.3	317	2 H72322	thioredoxin reduct
14	671	40.4	308	2 B97007	thioredoxine reduct
15	668	40.2	308	1 S23117	thioredoxine reduct
16	645.5	38.8	345	1 A53307	thioredoxin-disulf
17	644.5	38.8	322	1 A53307	thioredoxin reduct
18	643.5	38.7	336	2 D71016	thioredoxin-disulf
19	639.5	38.6	310	2 B97777	thioredoxin-disulf
20	639.5	38.5	335	2 A70851	thioredoxin-disulf
21	632.5	38.1	458	1 S77662	probable thioredox
22	626.5	37.7	322	2 T36577	thioredoxin reduct
23	619.5	37.3	310	2 D71703	thioredoxin reduct
24	605	36.4	351	2 B71556	probable thioredox
25	601	36.2	318	1 G64186	thioredoxin-disulf
26	599.5	36.1	303	1 E69194	thioredoxin-disulf
27	598.5	36.0	333	2 T41743	thioredoxin-disulf
28	595	35.8	311	2 B86530	thioredoxin reduct
29	595	35.8	311	2 C72093	thioredoxin reduct

30	593	35.7	312	2 C81710	thioredoxin reduct
31	591.5	35.6	483	2 AG1898	thioredoxin reduct
32	587.5	35.3	320	2 T42062	thioredoxin-disulf
33	584.5	35.2	535	2 T00824	probable thioredox
34	584	35.1	348	2 G87604	thioredoxin reduct
35	581.5	35.0	383	2 A84552	probable thioredox
36	579.5	34.9	333	1 S44027	thioredoxin-disulf
37	575	34.6	300	1 A69444	thioredoxin-disulf
38	573.5	34.5	320	2 AH0167	thioredoxin-disulf
39	570.5	34.3	362	2 D84281	thioredoxin limpor
40	569.5	34.3	321	1 RDECT	thioredoxin-disulf
41	569.5	34.3	321	2 E90750	thioredoxin reduct
42	569.5	34.3	321	2 C85614	thioredoxin reduct
43	564	33.9	307	2 A99601	thioredoxin reduct
44	563.5	33.9	322	2 AD0611	thioredoxin reduct
45	563	33.9	328	2 AF2081	thioredoxin reduct

ALIGNMENTS

RESULT 1

E89849
thioredoxine reductase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: E89849
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaico, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E89849
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-311 <KUR>
A:Cross-references: GB:BA000018; PID:gl3700655; PIDN:BA841952.1; GSPDB:GN00149
C:Genetics:
C:Gene: trxB
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 95.2%; Score 1582; DB 2; Length 311;
Best Local Similarity 99.4%; Pred. No. 2.9e-111;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	3	TEIDFDIAIIGAGPAGMTAAVYASPA	NLKTVMIERGIPGGQWANTEVEVFP	FGFEMITGP 62
Db	2	TEIDFDIAIIGAGPAGMTAAVYASPA	NLKTVMIERGIPGGQWANTEVEVFP	FGFEMITGP 61
QY	63	DLSTKMFHAKKFGAVYQYGD	IKSVEDKGEYKVINFGNKELTAKAVI	IATGAEYKKGVP 122
Db	62	DLSTKMFHAKKFGAVYQYGD	IKSVEDKGEYKVINFGNKELTAKAVI	IATGAEYKKGVP 121
QY	123	GEELGGRGVSYCAVCDGAF	FNKRLFVIGGDSAVEEGTFTTKFADK	VTVHRRDELRA 182
Db	122	GEELGGRGVSYCAVCDGAF	FNKRLFVIGGDSAVEEGTFTTKFADK	VTVHRRDELRA 181
QY	183	QRILQDRAFNKDKIDFTWSHT	TKSINEKDKGVSVTLTSTKDGSEET	HEADGVFYIGMK 241
Db	182	QRILQDRAFNKDKIDFTWSHT	TKSINEKDKGVSVTLTSTKDGSEET	HEADGVFYIGMK 241
QY	243	PLTAPFKDLGINTDVGIVT	KDDMTTSPVGI	FAAGDVREDKGLRQIVTATGSGS
Db	242	PLTAPFKDLGINTDVGIVT	KDDMTTSPVGI	FAAGDVREDKGLRQIVTATGSGS
QY	303	EYIEHLNDQA 312		
Db	302	EYIEHLNDQA 311		

RESULT 2

A69727
thioredoxin-disulfide reductase (EC 1.8.1.9) - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
C:Accession: A69727
R:Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, F.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Tognoni, A.; Tosato, V.; Uchiyama
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yoshikawa, H.; Danchin, A.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69727
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-316 <KUN>
A:Cross-references: GB:Z99121; GB:AL009126; NID:92635827; PIDN:CAB15484.1; PID:92635992
A:Experimental source: strain 168
C:Genetics:
A:Gene: trxB
C:Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
C:Function:
A:Description: catalyzes the reversible reduction of oxidized thioredoxin by NADPH
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology
C:Keywords: FAD; flavoprotein; homodimer; NADP; oxidoreductase; relox-active disulfide
F;3-305/Domain: thioredoxin reductase homology <TRXB>
F;8-36/Region: beta-alpha-beta FAD nucleotide-binding fold
F;147-174/Region: beta-alpha-beta NADP nucleotide-binding fold
F;135-138/Disulfide bonds: relox-active #status predicted

Query Match 69.6%; Score 1157; DB 1; Length 316;
Best Local Similarity 70.7%; Pred. No. 2.2e-79;
Matches 222; Conservative 33; Mismatches 59; Indels 0; Gaps 0;
Qy 1 MGTEIDFDIAGAGPAGMTAAVYASRANLTKVMIERGIPGGQMANTEVENFPGFEMI 60
Db 1 MSEKIDYDVIITAGPAGMTAAVYTSRANLTKVMIERGIPGGQMANTEVENFPGFEMI 60
Qy 61 GPDLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYKKG 120
Db 61 GPDLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYKKG 120
Qy 121 VPGEQLGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDL 180
Db 121 VPGEQLGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDL 180
Qy 181 RAQRILODRAFNKIDFIWHSHTTKSINEKDGKGVSVTLSTKDGSEBTHEADGVFIY 240
Db 181 RAQRILODRAFNKIDFIWHSHTTKSINEKDGKGVSVTLSTKDGSEBTHEADGVFIY 240
Qy 241 VPGEQLGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDL 300
Db 241 VPGEQLGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDL 300
Qy 301 AAEYIEHLNDQARS 314
Db 301 VQHYVEELQETLTK 314

RESULT 3
C84096
thioredoxin reductase (NADPH) trxB [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: C84096
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C84096
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <STO>
A:Cross-references: GB:AP001519; GB:BA000004; NID:910176109; PIDN:BAB07290.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: trxB
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 68.9%; Score 1145.5; DB 2; Length 315;
Best Local Similarity 68.6%; Pred. No. 1.6e-78;
Matches 216; Conservative 38; Mismatches 60; Indels 1; Gaps 1;
Qy 1 MGTEIDFDIAGAGPAGMTAAVYASRANLTKVMIERGIPGGQMANTEVENFPGFEMI 59
Db 1 MGTEIDFDIAGAGPAGMTAAVYTSRANLTKVMIERGIPGGQMANTEVENFPGFEMI 60
Qy 60 TGPDLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYK 119
Db 60 TGPDLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAEYK 120
Qy 120 GVPGEQLGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDE 179
Db 120 GVPGEQLGGRGVSYCAVCDGAFKFKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDE 180
Qy 181 LRAQRILODRAFNKIDFIWHSHTTKSINEKDGKGVSVTLSTKDGSEBTHEADGVFIY 239
Db 181 LRAQRILODRAFNKIDFIWHSHTTKSINEKDGKGVSVTLSTKDGSEBTHEADGVFIY 240
Qy 240 GMKPLTAPFKDLGITNDVGVIVTKDMMTTSVPGIFAGDVDRKGLRQIVTATGDSIAAQ 299
Db 240 GMKPLTAPFKDLGITNDVGVIVTKDMMTTSVPGIFAGDVDRKGLRQIVTATGDSIAAQ 300
Qy 300 SAAEYIEHLNDQARS 314
Db 301 NVQHYVEELAEKVK 315

RESULT 4
AH1759
thioredoxin reductase [imported] - Listeria innocua (strain Clipl1262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1759
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Wehland
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1759
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97848.1; PID:916415158; GSPDB:GN00178
A:Experimental source: strain Clipl1262
C:Genetics:
A:Gene: trxB
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 63.6%; Score 1057; DB 2; Length 319;
Best Local Similarity 65.8%; Pred. No. 7e-72;
Matches 200; Conservative 44; Mismatches 60; Indels 0; Gaps 0;
Qy 7 FDIAIAGPAGMTAAVYASRANLTKVMIERGIPGGQMANTEVENFPGFEMITGDLST 66

Db 8 YDVIIGAGPAGMTAALYTSRADLDTLMIERGVPGQWNTAEVNPFGDLSILGPDLS 67
 QY 67 KMFEHAKFGAVYQYGDVSKVEDKGYKVINFGNKELTAKAVIIATGAEYKIGVPGQEE 126
 Db 68 KMLSGAKQFGAEYAGYDKIVEIDGKEFTVYTAGSKTYKARAIITATGAHRKLGAAAGEE 127
 QY 127 LGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 186
 Db 128 LSGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 187
 QY 187 QDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMKPLTA 246
 Db 188 QDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMKPLTA 247
 QY 247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAQAQSAAYIE 306
 Db 248 AFLSLGITDDEGYIVTDEMRNLPGIFAAGDVDRKGLRQIVTATGDSIAQAQSAAYIE 307
 QY 307 HLND 310
 Db 308 ELKE 311

RESULT 5

AF1384
 thioeredoxin reductase [imported] - Listeria monocytogenes (strain EGD-e)
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C;Accession: AF1384
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
 A;Authors: Kneft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AF1384
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-319 <GLA>
 A;Cross-references: GB:NC_003210; PIDN:CAD00556.1; PID:gi6411966; GSPDB:GN00177
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: trxB
 C;Superfamily: thioeredoxin reductase; thioeredoxin reductase homology

Query Match 63.4%; Score 1054; DB 2; Length 319;
 Best Local Similarity 65.5%; Pred. No. 1.2e-71;
 Matches 199; Conservative 43; Mismatches 62; Indels 0; Gaps 0;

QY 7 FDIAIAGPAGMTAAYASRANLKTVMIERGIPGQWNTAEVNPFGDLSILGPDLS 67
 Db 8 YDVIIGAGPAGMTAALYTSRADLDTLMIERGVPGQWNTAEVNPFGDLSILGPDLS 67
 QY 67 KMFEHAKFGAVYQYGDVSKVEDKGYKVINFGNKELTAKAVIIATGAEYKIGVPGQEE 126
 Db 68 KMLSGAKQFGAEYAGYDKIVEIDGKEFTVYTAGSKTYKARAIITATGAHRKLGAAAGEE 127
 QY 127 LGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 186
 Db 128 LSGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 187
 QY 187 QDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMKPLTA 246
 Db 188 QDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMKPLTA 247
 QY 247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAQAQSAAYIE 306
 Db 248 AFLSLGITDDEGYIVTDEMRNLPGIFAAGDVDRKGLRQIVTATGDSIAQAQSAAYIE 307
 QY 307 HLND 310

Db 308 ELKE 311

RESULT 6

D86742
 thioeredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Lactococcus lactis subsp. lac.
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Jun-2002
 C;Accession: D86742
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich, Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s.
 A;Accession: D86742
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <STO>
 A;Cross-references: GB:AE005176; PID:gl2723976; PIDN:AAK05038.1; GSPDB:GN00146
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: trxB1
 C;Superfamily: thioeredoxin reductase; thioeredoxin reductase homology
 C;Keywords: oxidoreductase

Query Match 52.5%; Score 872; DB 2; Length 308;
 Best Local Similarity 53.1%; Pred. No. 5e-58;
 Matches 163; Conservative 54; Mismatches 90; Indels 0; Gaps 0;

QY 3 TEIDPDIAIAGPAGMTAAYASRANLKTVMIERGIPGQWNTAEVNPFGDLSILGPDLS 62
 Db 2 TEKYDVIIIGSGPAGMTAAYASRANLKTVMIERGIPGQWNTAEVNPFGDLSILGPDLS 61
 QY 63 DLSTKMEHAKFGAVYQYGDVSKVEDKGYKVINFGNKELTAKAVIIATGAEYKIGV 122
 Db 62 ELSMKMAEPLGIGVENAGFVTAIEDHGYKKIITDEDFVTKSIIIIATGANHRKLETP 121
 QY 123 GRQELGGRGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRA 182
 Db 122 GEEYGARGVSYCAVCDGGAFFKNKRLFVIGGSDSAVEEGTFTTKFADKVTIVHRRDELRA 181
 QY 183 QRILQDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMK 242
 Db 182 QELIQDRAFKNDKIDFIWHTTKSINEKDGKVGSVTLSTKDGSEETHADGVFIYIGMK 241
 QY 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAQAQSA 302
 Db 242 PVAEFAGNLGITDEAGWIITDDHMETSLPGIPAVGDEVKQDFRQITTAIGDGAQAQAEAY 301
 QY 303 EYIEHLN 309
 Db 302 KFAVELD 308

RESULT 7

G98035
 thioeredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Streptococcus pneumoniae
 C;Species: Streptococcus pneumoniae
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
 C;Accession: G98035
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Bargett, S.; DeGoff, B.S.; Ee, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M. Y. P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A97872; MUID:21429245; PMID:11544234
 A;Accession: G98035
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-303 <KUR>
 A;Cross-references: GB:AE007317; PIDN:AAL00116.1; PID:gl5458956; GSPDB:GN00174
 C;Genetics:

A:Gene: trxB
C:Superfamily: thioredoxin reductase; thioredoxin reductase homology
C:Keywords: oxidoreductase

Query Match	51.2%;	Score	851;	DB	2;	Length	303;
Best Local Similarity	54.0%;	Pred.	No.	1.9e-56;			
Matches	163;	Conservative	55;	Mismatches	82;	Indels	2;
Gaps							2;
Qy	7	FDIAIIGAGPAGMTAAVYASRANLKTVMIERIGPGQMANTEEVENPFGEFMITGPOLST	66				
Db	2	YDTIIIGAGPAGMTAALYAASNLKVALIEGLPGQMNTSDIENPYGANISGPELAÆ	61	:	:	:	:
		: :		:	:	:	:
Qy	67	KMFÈHAKKFAGVYOYGDIKSVEDRGKEYKVINFGNKELTAKAVIIATGAAYKKIGVPGBQE	126	:	:	:	:
Db	62	KMFEPLENLGVHEHYGVYVENVEDHGDFPKVMTDQTYETRTVI VATSGSKHRPLGVPGBEE	121	:	:	:	:
		: :		:	:	:	:
Qy	127	LGGRGVSVCACDGCAFFKNKELFVIGGDSAVEEGCTFTTKADKVTIVHRRDELRACORIL	186	:	:	:	:
Db	122	LNSRGVSVCACDGCAFFDQLLVGGGDSAVEEALFLTRFAKVTIVHRRDQLRAQKWL	181	:	:	:	:
		: :		:	:	:	:
Qy	187	QDRAFKNDKIDFIWSHTTKSINEKDKGVSVTLTSTKDGSBETHADGVFIYGMKP.LTA	246	:	:	:	:
Db	182	QDRAPANEKISFIWDSUVKEI-KGENRVSVVFENVKQTGYTEQAQFGGVFIYVGDLPLSD	240	:	:	:	:
		: ~:		:	:	:	:
Qy	247	PFKDLGIENDVGYIVTKDDMTTSVPGIIFAGDVVRDKGLRIQVITATGDGSIAAQSAAEYI-	305	:	:	:	:
Db	241	FVKELNIQDAQGWIVTDSHMKTAVDGI FAVGDVRLKDLRQVTTAVDGDGAIAGQEA YKFI	300	:	:	:	:
		: ~:		:	:	:	:
Qy	306	BH	307				
Db	301	EH	302				

RESULT 8

G95169
thioredoxin reductase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: G95169
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75552.1; PID:g14972947; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4

C; Gene: SP1458
C; Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match	51.1%;	Score 849;	DB 2;	Length 303;
Best Local Similarity	53.6%;	Pred. No. 2.6e-56;		
Matches 162;	Conservative 57;	Mismatches 81;	Indels 2;	Gaps 2
QY	7	FDIAIIIGAGPAGMTAAVYASRANLKVTMIERGIPGGOMANTEEVNFFGPEMITGPDLSLT	66	
Db	2	YDTIIIGAGPAGMTAAVYASRANLKVALIEGGLPGGMNTSDIENYFPGYANISPELAE	61	
QY	67	KMFPHAKFGAVYQGDITKTSVEDGEYKVINFGNKELTAKAVIIATGAYKKIGVPGQEE	126	
Db	62	KMFEPLENLGVHEIYGYVYVENEDHGDFFKVMWDDQTYETRTVVAVSGSKHRLGVPGGEE	121	
QY	127	LGGRGVSYCAVCDGGAFFKFKRLFVITGGGDSAVEEGTFTTKFADKVTIYHRRDELRAQRL	186	
Db	122	LNSRGVSYCAVCDGGAFFRDQDLLVVGGGDSAVEEALFLTRPAKVTIYHRRDOLRAQKVL	181	
QY	187	QDRAPFNKDIDFIWSHHTTKSINEKKGVSVLTLSITKGGSETHADGVETIYIGMKPLTA	246	

RESULT 10

thioredoxin-disulfide reductase (EC 1.8.1.9) - Eubacterium acidaminophilum D35156
N:Alternate names: dihydrolipoamide dehydrogenase [misidentification]
S:Species: Eubacterium acidaminophilum
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
C:Accession: S38988 D35156
R:Luebers, M.; Andreessen, J.R.
Eur. J. Biochem. 217, 791-798, 1993

Db	182	QDRAPANEKISFIWDSVVREI-KGENRVESVVFENVKIQVTEQAGGVFIYVGLDPLSD	240
Qy	247	PKPDIGIITNDVGYIVTKDDMTTSVPGIFAGSDVRDKGLRQIVTATGDGSIAAQSAEYI-	305
Db	241	FVKELNIQDQAGWIVTDNHEMTKTDVGIFAVGDVRLKDLRQVTTAVDGAIGAEYKFIIT	300
Qy	306	EH 307	
Db	301	EH 302	

RESULT 9

A75330
thioredoxin reductase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75330
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75330
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <WHI>
A:Cross-references: GB:AE02036; GB:AE00513; NID:G6459766; PIDN:AAF11534.1; PID:G6459766
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1982
A:Map position: 1
C:Cross-referenced family: thioredoxin reductase: thioredoxin reductase homology

Query Match	43.8%	Score 728.5	DB.2	Length 325;
Best Local Similarity	48.4%	Pred. No. 3.1e-47;		
Matches 152; Conservative	51;	Mismatches 100;	Indels 11;	Gaps 4
QY	3	TEIDFDIAIICAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEEVNPGF-EMITG	61	
DB	5	TAHYDVMVILGGPAGLTAIYITGRAQLSTLILEKMGEGQIANSEEVNPGFPEPIAG	64	
QY	62	PDLSTKMPHAKFKGAVTYQYGDIIKSVEDKGYYKVINFG---NKELTAKAVIATGAEYK	117	
DB	65	MELAQRMHQAEKFGAKVEMDEBVGQVQHDATSHPYPTFVRGYNGEYRAKAVILATGADPR	124	
QY	118	KIGVPGGEELGGRGVSYCAVCDGAPFKNRLFVIGGGDSAAVEEGFTTKADKVTIYVHR	177	
DB	125	KLIGPGEDNFMKGYSTCATCDGFFYKGGKVVVIGGGDAAAVEEGMFLTKFADEVITVHR	184	
QY	178	DELRAQRILQDRAFNKDKI DFIWSHTTKSINEKDGKGVSVTITSTPKDGESETHEADGVFI	237	
DB	185	DTLRANKVAQARAFAFNPKKFLIWDTA VAEI QCAD-SVSGVKLRNLKGTGEVSELATDGVFI	243	
QY	238	YIGMKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFPAAGDVDRDKGLRQIVTATGGGSA	297	
DB	244	FIGHVPNTAFVKD TVSLRDDGVYDVRDEIYTNIPMLFAAGDVSDYIYROLATSVAGTRA	303	
QY	298	A-----QSAAEYIE	306	
DB	304	AMWTERQLAALEVE	317	

A:Title: Components of glycine reductase from Eubacterium acidaminophilum. Cloning, sequ
 A:Reference number: S3988; MUID:94039119; PMID:8223622
 A:Accession: S3988
 A:Molecule type: DNA
 A:Residues: 1-315 <LUE>
 A:Cross-references: GB:L04500; NID:g2708733
 R:Dieterichs, D.; Meyer, M.; Schmidt, B.; Andreesen, J.R.
 J. Bacteriol. 172, 2088-2095, 1990
 A:Title: Purification of NADPH-dependent electron-transferring flavoproteins and N-termi
 A:Reference number: A35156; MUID:90202731; PMID:2319809
 A:Accession: D35156
 A:Molecule type: protein
 A:Residues: 1-33, 'X', 35-46, 'X', 48, 'D', 50-55 <DIE>
 A:Note: the designation "atypically small dihydrolipoamide dehydrogenase" was revised in
 C:Genetics:
 A:Gene: trxB
 A:Start codon: GTG
 C:Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
 C:Function:
 A:Description: catalyzes the reversible reduction of oxidized thioredoxin by NADPH
 C:Superfamily: thioredoxin reductase; thioredoxin reductase homology
 C:Keywords: FAD; flavoprotein; homodimer; NADP; oxidoreductase; redox-active disulfide
 F:1-309/Domain: thioredoxin reductase homology <TRXB>
 F:6-34/Region: beta-alpha-beta FAD nucleotide-binding fold
 F:146-173/Region: beta-alpha-beta NADP nucleotide-binding fold
 F:134-137/Disulfide bonds: redox-active #status predicted
 Query Match 43.7%; Score 726; DB 1; Length 315;
 Best Local Similarity 49.8%; Pred. No. 4.6e-47;
 Matches 153; Conservative 50; Mismatches 96; Indels 8; Gaps 3;
 QY 7 FDIATIGAGPAGMTAAVYASRANKVTMIERGIPGGQMANTEEVENPPG-FEMITGPDLS 65
 Db 5 YDLAIIGSGPAGLAALYGARAKMTIMIEGQKVGQIVITHEVANYPGSVREATGPSLI 64
 QY 66 TKMFEHAKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIATGAAYKKIGVPGSQ 125
 Db 65 ERMEEQANFGEAKVMDKIVDVLQDKIKVIGKEAEYKAKSVILATGAAPRLAGCPGQ 124
 QY 126 ELGGRGVSYCAVCDGAFKFKKELFVIGGDSVAEEGTFTTKADKVTIVHRRDELRAQRI 185
 Db 125 ELTGKGVSYCATCDADFFEDMEVFVGGDTAVEEAMYLAKFARKVTIVHRRDELRAAKS 184
 QY 186 LQDRAFKNDKIDPIWSHHTKTSINEKDKGVSVTLTSTKDG-----VLTSTKDGSEETHEADGVFIYI 239
 Db 185 IQEKAFKPKLDPMNSALEEI-KGDGIVESAVFKNLVTGETTEYFANEEDGTGFIYFI 243
 QY 240 GMKPLTAPDKLGTNDVGYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAAQ 299
 Db 244 GYIPKSDVFKGKITLDDAGYIITDNNMTNVDGVFAAGDIRVKSRLQVVVTACADGAIAAT 303
 QY 300 SAAEYIE 306
 Db 304 QAEKYVE 310
 RESULT 11
 S63990
 N:Alternative names: glycine reductase complex Clostridium litorale
 C:Species: Clostridium litorale
 C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
 R:Kreimer, S.; Andreesen, J.R.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: S63990
 A:Accession: S63990
 A:Molecule type: DNA
 A:Residues: 1-315 <KRE>
 A:Cross-references: EMBL:U24268; NID:g1171124; PIDN:AAC43575.1; PID:g1171125
 Eur. J. Biochem. 234, 192-199, 1995
 A:Title: Glycine reductase of Clostridium litorale. Cloning, sequencing, and molecular a

A:Reference number: S63987; MUID:96096738; PMID:8529640

A:Accession: S63989

A:Molecule type: DNA

A:Residues: 1-117 <XRW>

A:Cross-references: EMBL:U24268; NID:g1171124

C:Genetics:

A:Gene: trxB

A:Start codon: GTG

C:Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
 C:Function:

A:Description: catalyzes the reversible reduction of oxidized thioredoxin by NADPH
 C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

C:Keywords: FAD; flavoprotein; homodimer; NADP; oxidoreductase; redox-active disulfide

F:1-309/Domain: thioredoxin reductase homology <TRXB>

F:6-34/Region: beta-alpha-beta FAD nucleotide-binding fold

F:146-173/Region: beta-alpha-beta NADP nucleotide-binding fold

F:134-137/Disulfide bonds: redox-active #status predicted

Query Match 42.5%; Score 706; DB 1; Length 315;

Best Local Similarity 48.5%; Pred. No. 1.5e-45;

Matches 150; Conservative 53; Mismatches 98; Indels 8; Gaps 3;

QY 7 FDIATIGAGPAGMTAAVYASRANKVTMIERGIPGGQMANTEEVENPPG-FEMITGPDLS 65

Db 5 YDLAIIGSGPAGLAALYGARAKMTLLLEGKVGQIVITHEVANYPGSVPEATGPSLI 64

QY 66 TKMFEHAKFGAVYQYGDIKSVDEKGEYKVINFGNKELTAKAVIATGAAYKKIGVPGSQ 125

Db 65 GRMEEQVEFGAERVMDNIVDFTDKIKVKGAKGEYKAKAVIATGASPPLAGCPGEK 124

QY 126 ELGGRGVSYCAVCDGAFKFKKELFVIGGDSVAEEGTFTTKADKVTIVHRRDELRAQRI 185

Db 125 ELTGKGVSYCATCDADFFEDMEVFVGGDTAVEEAMLTKEARKVTIVHRRDELRAAKS 184

QY 186 LQDRAFKNDKIDPIWSHHTKTSINEKDKGVSVTLTSTKDG-----SEETHEADGVFIYI 239

Db 185 IQEKAFKPKLDMNMTVIEEI-KGDGIVESAVFKNRTEGTEVFAPEEDGTGFIYFI 243

QY 240 GMKPLTAPDKLGTNDVGYIVTKDDMTTSVPGIFAAGDVDRKGLRQIVTATGDSIAAQ 299

Db 244 GYDPKLSALVEGKLELDETYGIFTDNNMTNVEGVFAAGDIRVKSRLQVVVTATADGAIAAV 303

QY 300 SAAEYIEHL 308

Db 304 QAEKYIEEL 312

RESULT 12

C71278

probable thioredoxin reductase (trxB) - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999

C:Accession: C71278

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDO

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: C71278

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-307 <COL>

A:Cross-references: GB:AE001252; GB:AE000520; NID:g3323119; PIDN:AAC65780.1; PID:g332312

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0814

C:Superfamily: thioredoxin reductase; thioredoxin reductase homology

F:1-302/Domain: thioredoxin reductase homology <TRXB>

Query Match

Best Local Similarity 42.0%; Score 697.5; DB 2; Length 307;

Matches 142; Conservative 55; Mismatches 108; Indels 3; Gaps 3;

QY 4 EIDEDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEVENFPGFEM-ITGP 62
 DB 2 ETDYDVIIVGAAGLSAAQYACRANLRLTVIESAHGQALLIDSLNENPGYATPISGF 61
 QY 63 DLSTKMFHAKKFGAVYQYD1KSVDEKGEYKVINFGNKELTAKAVIATGAEYKIGVP 122
 DB 62 EYAEENMKQAVAFGAQIAVEEVTITGKRDSVPHITTTGTGAYTAMSVILATGAHRKMGIP 121
 QY 123 GQELGGRGVSCAVCDGGAFFKPKRLFTVIGGDSAVEEGTFTTKPADKVTIVHRRDELRA 182
 DB 122 GESEFLGRGVSCATCDGPFPRKXHVIVVGGDAACDESILVSLRDLTDRVTMHRDLRA 181
 QY 183 ORLQDRAFNKDKIDFIWHSHTTKSINEXDKGVSVTLTSTKDGSEETHADGVFIYGMK 242
 DB 182 QXAIARTLKNPHIAVQWNTLLEAV-RGETKVSSVLLKDVKTGETRELACDAVFFIIGMV 240
 QY 243 PLTAPFKDLGITNDVGVIVTKDMMTSVPOIFPAAGDVDRKGLRQIVTATGDSIAQSA 302
 DB 241 PITGLLPD-AEKDSTGYIVTDDMTSVEGIFPAAGDVRAKSFQVITATSDGALAHA 299
 QY 303 EYIEHLND 310
 DB 300 SYIDTLQN 307

RESULT 13
 H72322
 thioeredoxin reductase - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: H72322
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: H72322
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-317 <ARN>
 A:Cross-references: GB:AE001753; GB:AE000512; NID:G4981397; PIDN:AA035951.1; PID:G498140
 A:Experimental source: strain MSB8
 C:Genetics:
 C:Gene: TM0869
 C:Superfamily: thioeredoxin reductase; thioeredoxin reductase homology
 F:14-316/Domain: thioeredoxin reductase homology <TRXB>
 Query Match 41.3%; Score 687; DB 2; Length 317;
 Best Local Similarity 44.8%; Pred. No. 3.9e-44;
 Matches 134; Conservative 63; Mismatches 100; Indels 2; Gaps 2;
 QY 7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEVENFPGFEMITGPDLST 66
 DB 18 YDIVVVGPGAGLSAIVARRAGLSVLVVEKAIEGGYVNLTHLVENPGFPFPAISGEELAS 77
 QY 67 KMFHAKKFGAVYQYD1KSVDEKGEYKVINFGN-KELTAKAVIATGAEYKIGVPGEQ 125
 DB 78 KPEHAERKFGADIVNVEVVKLVQGGKVVLDLDDGRIEAPVIVATGANPKLVNVEGK 137
 QY 126 ELGGRGVSCAVCDGGAFFKPKRLFTVIGGDSAVEEGTFTTKPADKVTIVHRRDELRAQRI 185
 DB 138 EFPFGKGVSCATCDGYLFAKGKIVVVGGSADDESIFLSNVNKTIMTQLLETLTA 197
 QY 186 LQDRAFNKDKIDFIWHSHTTKSINEXDKGVSVTLTSTKDGSEETHADGVFIYGMKPLT 245
 DB 198 LQERVLNPKIEVYNSVREIRGKD-KVEEVVIVNKTGETKVLKADGVFIIGLDPS 256
 QY 246 APFKDLGITNDVGVIVTKDMMTSVFGIFPAAGDVDRKGLRQIVTATGDSIAQSAAY 304
 DB 257 KLEGLVELDPYGVIVTDENNETSVKGIYAVGVDRKKNLQIVTVADGAIAVEHA 315

RESULT 14
 B97007
 thioeredoxine reductase [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: B97007
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: B97007
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-308 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK78845.1; PID:G15023764; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 C:Gene: CAC0869
 C:Superfamily: thioeredoxin reductase; thioeredoxin reductase homology
 Query Match 40.4%; Score 671; DB 2; Length 308;
 Best Local Similarity 42.2%; Pred. No. 6e-43;
 Matches 130; Conservative 74; Mismatches 102; Indels 2; Gaps 2;
 QY 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQWANTEVENFPGFEMIT 60
 DB 1 MKKEKILDLVILGAGPAGLTAGIYSSRAKLDFIILENLVGGQIRETPSIENPGFDSIS 60
 QY 61 GPDLSTKMFHAKKFGAVY-QYD1KSVDEKGEYKVINFGNKELTAKAVIATGAEYK 119
 DB 61 GADLADKMQEHAEKAGAVIDEFGNITSVKLTDEKIFETSDTIYKPSKVIATGSKRPL 120
 QY 120 GVPGEQLGGRGVSCAVCDGGAFFKPKRLFTVIGGDSAVEEGTFTTKPADKVTIVHRRDE 179
 DB 121 VPVEEKKLRGKGIHICELCDGAGVDKDIIVVGGNSAIDAAIFLTAKYAKNLTVVHRSEK 180
 QY 180 LRAQRIILQDRAFNKDKIDFIWHSHTTKSINEXDKGVSVTLTSTKDGSEETHADGVFIYI 239
 DB 181 LRAEMRSQDELFEKNVYKLLNLTQIKHV-EGENSIENIVLENSKTGKSLKADAIYVI 239
 QY 240 GMKELTAPFKDLGITNDVGVIVTKDMMTSVPGIFPAAGDVDRKGLRQIVTATGDSIAAQ 299
 DB 240 GTMPEKTELKFDIDLTELGHKIKTNENLETNIKGVFAAGDVREKIRQLTTAVNDGSIASL 299
 QY 300 SAABYIEH 307
 DB 300 MAEKYIRN 307
 RESULT 15
 S29117
 thioeredoxin-disulfide reductase (EC 1.8.1.9) - Clostridium pasteurianum
 C:Species: Clostridium pasteurianum
 C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
 C:Accession: S29117
 R:Mathieu, I.; Meyer, J.; Moulis, J.M.
 Biochem. J. 285, 255-262, 1992
 A:Title: Cloning, sequencing and expression in Escherichia coli of the rubredoxin gene
 A:Reference number: S29117; MUID:92344580; PMID:1637309
 A:Accession: S29117
 A:Molecule type: DNA
 A:Residues: 1-308 <MAT>
 A:Cross-references: EMBL:M60116; NID:G144905; PIDN:AAA23276.1; PID:G144906
 C:Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
 C:Function:
 C:Description: catalyzes the reversible reduction of oxidized thioeredoxin by NADPH
 C:Superfamily: thioeredoxin reductase; thioeredoxin reductase homology
 C:Keywords: FAD; flavoprotein; homodimer; NADP; oxidoreductase; redox-active disulfide
 F:3-305/Domain: thioeredoxin reductase homology <TRXB>
 F:8-36/Region: beta-alpha-beta FAD nucleotide-binding fold
 F:148-175/Region: beta-alpha-beta NADP nucleotide-binding fold

F:136-139/Disulfide bonds: redox-active #status predicted

Query Match 40.2%; Score 668; DB 1; Length 308;
Best Local Similarity 43.8%; Pred. No. 1e-42;

Matches 134; Conservative 64; Mismatches 106; Indels 2; Gaps 2;

QY	1	MGTEIDFDIALIGAPAGMTAAVYASRANLKTVMIERGIPGQOMANTEEVENFPFGFEMIT	60
Db	1	MKEEKQLDLVIIGAGPAGLTAAYAIRAKLNTLVLENELVGGQIRETYTVENFPFGFNVIS	60
QY	61	GPDLSTKWEHAKKFGA-VVOYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKXI	119
Db	61	GADLADKWEHAAISIGNIDQFSNIEKIKLSDDEKIIETEDVIYKVKALIIATGAKSRL	120
QY	120	GVPGQELGGRGVSYCAVCDGAFKPKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDE	179
Db	121	PIPEEEKLHGKVIHYCELCGALYQGRDLVVVGGNSAVEAAFLTXYARNITIVHQFDY	180
QY	180	LRAQRILQDRAFKNDKIDFTWSHTTKSINEKDGKVGSVTLTSTKOGSEETHEADGVFIYI	239
Db	181	LQAKQYSQDELFKHKNVKIWDSEIRNI-VGENEIEKIVVENVKTKOKTELKADGVFVYI	239
QY	240	GMKPLTAPPKDLGITNDVGVIYTKDDMTTSVPGIFAAGDYRDKGLRQIVTATGDSIAAQ	299
Db	240	GYPEKTELFKDSININKWGIETDENMETNKGVFAGDVRSKLIIRQLTTAVSDGTVAAAL	299
QY	300	SAAEYI 305	
Db	300	MAEKYI 305	

Search completed: September 15, 2004, 12:21:32
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:05:08 ; Search time 23 Seconds
(without alignments)
724.454 Million cell updates/sec

Title: US-09-825-212-1
Perfect score: 1662
Sequence: 1 MGTEIDFDIAIAGGAGMT.....AABVIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1582	95.2	311	1	TRXB_STAAM
2	1455	87.5	310	1	TRXB_STAEP
3	1154	69.4	315	1	TRXB_BACSU
4	1057	63.6	319	1	TRXB_LISIN
5	1054	63.4	319	1	TRXB_LISMO
6	726	43.7	315	1	TRXB_BUBAC
7	706	42.5	315	1	TRXB_GLOLI
8	697.5	42.0	307	1	TRXB_TREPA
9	668	40.2	308	1	R34K_CLOPA
10	644.5	38.8	321	1	TRXB_STRCL
11	641.5	38.6	310	1	TRXB_RICCN
12	639.5	38.5	335	1	TRXB_MYCTU
13	632.5	38.1	458	1	TRXB_MYCLE
14	625.5	37.6	321	1	TRXB_STRCO
15	619.5	37.3	310	1	TRXB_MYCSM
16	619.5	37.3	311	1	TRXB_RICPR
17	605	36.4	312	1	TRXB_HLTR
18	601	36.2	318	1	TRXB_HAEIN
19	598.5	36.0	333	1	TRBL_ARATH
20	595	35.8	311	1	TRXB_CHLPN
21	593	35.7	312	1	TRXB_CHLMU
22	581.5	35.0	383	1	TRB2_ARATH
23	564.5	34.0	320	1	TRXB_COXBU
24	564.5	34.0	320	1	TRXB_ECOLI
25	564	33.9	307	1	TRXB_MYCRU
26	558	33.6	311	1	TRXB_HELPU
27	558	33.6	318	1	TRXB_VIBCH
28	554	33.3	311	1	TRXB_HELPY
29	552	33.2	319	1	TRXB_BUCAP
30	551.5	33.2	318	1	TRBL_YEAST
31	550.5	33.1	315	1	TRXB_MYCGE
32	545.5	32.8	309	1	TRXB_UREPA
33	544.5	32.8	334	1	TRXB_NEURC

34 542.5 32.6 315 1 TRXB_MYCPN
35 526.5 31.7 342 1 TRB2_YEAST
36 510 30.7 319 1 TRXB_BUCAI
37 505.5 30.4 322 1 TRXB_SCHPO
38 505.5 30.4 333 1 TRXB_PENCH
39 493.5 29.7 326 1 TRXB_BORBU
40 491.5 29.6 326 1 TRXB_BUCBP
41 484 29.1 509 1 DHNA_BACSU
42 478.5 28.8 520 1 AHPE_PSEPK
43 466 28.0 305 1 TRXB_SPIBA
44 466 28.0 507 1 AHPE_STAAM
45 461.5 27.8 519 1 DHNA_BACSP

ALIGNMENTS

RESULT 1

TRXB_STAAM
ID TRXB_STAAM STANDARD; PRT; 311 AA.
AC Q99VL2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Thioedoxin reductase (EC 1.8.1.9) (TRXR).
GN TRXB OR SAV0764 OR SA0719 OR MW0726.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.";
RL Lancet 357:1225-1240 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
RN [3]
CC -!- CATALYTIC ACTIVITY: Thioedoxin + NADP(+) = thioedoxin disulfide + NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.

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EMBL; AP003360; BAB56926.1; -.

Wed Sep 15 13:38:57 2004

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DR EMBL; AP003131; BAB41952.1; -.
DR EMBL; AP004824; BAB94591.1; -.
DR PIR; E89849; E89849.
DR HSP; Q39243; 1VDC.
DR SWISS-2DPAGE; Q99VL2; STAA.
DR InterPro; IPR000759; Adnrx_reductase.
DR InterPro; IPR001327; FAD_Pyr_redux.
DR InterPro; IPR00103; Pyridine_redux_2.
DR InterPro; IPR008255; Pyr_redux2_AS.
DR InterPro; IPR005982; Thioredux_reduct.
DR Pfam; PF00070; Pyr_redux; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00469; PNDRTASEII.
DR TIGRFS; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
DR Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW Complete proteome. 42 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 35 137 REDOX-ACTIVE (BY SIMILARITY).
FT DISULFID 134 137 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 277 286 FAD (FLAVIN PART) (BY SIMILARITY).
SQ SEQUENCE 311 AA; 33616 MW; 1A337DE3736C9265 CRC64;

Query Match 95.2%; Score 1582; DB 1; Length 311;
Best Local Similarity 99.4%; Pred. No. 3.1e-107; Indels 0; Gaps 0;
Matches 308; Conservative 0; Mismatches 2;

QY 3 TEIDFDIAGPAGMTAAVYASRANKVTMIERGIPGGOMANTEVENPFGFEMITGP 62
Db 2 TEIDFDIAGPAGMTAAVYASRANKVTMIERGIPGGOMANTEVENPFGFEMITGP 61
QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAAYKKIGVP 122
Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAAYKKIGVP 121
QY 123 GEQELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRA 182
Db 122 GEQELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRA 181
QY 183 QRILQDRAFNKDKIDFIWSHTTKSINERKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMK 242
Db 182 QRILQDRAFNKDKIDFIWSHTTKSINERKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMK 241
QY 243 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAAGVDVRDKGLRQIVTATGDSIAAQA 302
Db 242 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAAGVDVRDKGLRQIVTATGDSIAAQA 301
QY 303 EYIEHLNDQA 312
Db 302 EYIEHLNDQA 311

RESULT 2
TRXB_STREP STANDARD; PRT; 310 AA.
ID TRXB STREP STANDARD; PRT; 310 AA.
AC Q8CFY8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN TRXB OR SE0547.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qian Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
Staphylococcus epidermidis strain (ATCC 12228).";

Mol. Microbiol. 49:1577-1593 (2003).
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
+ NADPH.
-!- COFACTOR: Binds 1 FAD per subunit (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
oxidoreductase family.

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or send an email to license@isb-sib.ch).

EMBL; AE016745; AA004144.1; -.
InterPro; IPR000759; Adnrx_reductase.
InterPro; IPR001327; FAD_Pyr_redux.
InterPro; IPR00103; Pyridine_redux_2.
InterPro; IPR008255; Pyr_redux2_AS.
InterPro; IPR005982; Thioredux_reduct.
Pfam; PF00070; Pyr_redux; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
PRINTS; PR00469; PNDRTASEII.
TIGRFS; TIGR01292; TRX_reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW Complete proteome. 42 FAD (ADP PART) (BY SIMILARITY).
NP_BIND 35 137 REDOX-ACTIVE (BY SIMILARITY).
DISULFID 134 137 FAD (FLAVIN PART) (BY SIMILARITY).
NP_BIND 277 286 FAD (FLAVIN PART) (BY SIMILARITY).
SEQUENCE 310 AA; 33544 MW; D5D6853667137D88 CRC64;

Query Match 87.5%; Score 1455; DB 1; Length 310;
Best Local Similarity 90.3%; Pred. No. 4.6e-98;
Matches 278; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 3 TEIDFDIAGPAGMTAAVYASRANKVTMIERGIPGGOMANTEVENPFGFEMITGP 62
Db 2 TEIDFDIAGPAGMTAAVYASRANKVTMIERGIPGGOMANTEVENPFGFEMITGP 61
QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAAYKKIGVP 122
Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGYKVINFGNKELTAKAVIATGAAYKKIGVP 121
QY 123 GEQELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRA 182
Db 122 GEQELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRA 181
QY 183 QRILQDRAFNKDKIDFIWSHTTKSINERKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMK 242
Db 182 QRILQDRAFNKDKIDFIWSHTTKSINERKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMK 241
QY 243 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAAGVDVRDKGLRQIVTATGDSIAAQA 302
Db 242 PLTAPFKDLGITNDVGIVTKDDMTTSVPGIFAAAGVDVRDKGLRQIVTATGDSIAAQA 301
QY 303 EYIEHLND 310
Db 302 EYIEHLND 309

RESULT 3
TRXB_BACSU STANDARD; PRT; 315 AA.
ID TRXB BACSU STANDARD; PRT; 315 AA.
AC P80880; O06971;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

```

Thioredoxin reductase (EC 1.8.1.9) (TRXR) (General stress protein 35) (GSP35).

GN TRXB OR BSU34790.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RC Denizot F.;

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RC MEDLINE=98044033; PubMed=9384377;

RX Kunze F., Ogasawara N., Moser I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Chai S.K., Codani J.J., Connerth I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferraci E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G., Guiseppe G., Guy B.J., Haga K., Halech E.J., Harwood C.R., Henaut A., Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaere-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K., Takeuchi M., Takakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";

RT Nature 390:249-256(1997).

RL [3]

RN SEQUENCE OF 1-23.

RP STRAIN=168 / IS59;

RC MEDLINE=97443988; PubMed=9298659;

RX Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U., Hecker M.;

RA "First steps from a two-dimensional protein index towards a response-regulation map for Bacillus subtilis.";

RL Electrophoresis 18:1451-1463(1997).

CC -1- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide + NADPH.

CC -1- COFACTOR: Binds 1 PAD per subunit (By similarity).

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- INDUCTION: By heat shock, salt stress, oxidative stress, glucose limitation and oxygen limitation.

CC -1- MISCELLANEOUS: The active site is a redox-active disulfide bond (By similarity).

CC -1- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.

CC

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RC STRAIN-CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rueniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Kurapkat G.,
RA Jones L.-M., Kaerst U., Kuhn M., Kunst F., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC
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CC
CC EMBL; AL596173; CAC97848.1; -
CC PUR; AH1759; AH1759.
CC ListList; LIN02621; -
CC InterPro; IPR000759; Adrndx_reductase.
CC InterPro; IPR001327; FAD_Pyr_redox.
CC InterPro; IPR001100; Pyr_redox.
CC InterPro; IPR008255; Pyr_redox2_AS.
CC InterPro; IPR000103; Pyridine_redox_2.
CC InterPro; IPR005982; Thioredox_reduct.
CC Pfam; PF00070; Pyr_redox; 1.
CC PRINTS; PR00419; ADXRTASE.
CC PRINTS; PR00368; FADPNR.
CC PRINTS; PR00411; PNRDRTASE1.
CC PRINTS; PR00469; PNRDRTASEII.
CC TIGRFAMs; TIGR01292; TRX_reduct; 1.
CC PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
CC Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW Complete proteome.
FT NP BIND 37 44 FAD (ADP PART) (BY SIMILARITY).
FT DISULFID 136 139 REDOX-ACTIVE (BY SIMILARITY).
FT NP BIND 279 288 FAD (FLAVIN PART) (BY SIMILARITY).
FT SEQUENCE 319 AA; 34244 MW; C77D54A952526CC1 CRC64;
SQ
Query Match 63.6%; Score 1057; DB 1; Length 319;
Best Local Similarity 65.8%; Pred. No. 2.6e-69;
Matches 200; Conservative 44; Mismatches 60; Indels 0; Gaps 0;
QY 7 FDIATIGAGPAGMTAAVYASRANLKTVMTERGIPGGQMANTEVEVFPFGFEMITGPDLSL 66
DB 8 YDVIILGAGPAGMTAAVYASRANLKTVMTERGIPGGQMANTEVEVFPFGFEMITGPDLSL 67
QY 67 KMFHAKFGAVYQYQDIKSVEDKGYKVINFGNKLTAQVITATGAGYKLGVPGEQF 126
DB 68 KMLSGAKQFGAEYAGDIKEVIDGKEFTVTAGSKTYKARIIATGAHRKLGAGESE 127
QY 127 LGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRAQRIL 186
DB 128 LSGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRAQRIL 187
QY 187 QDRAFKNDKIDFTWSHTTKSINEKDGKGVSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246

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Db 188 QDRAFKDEKVDPIWNTVVEIIGDGKKVTUKLVSTVDGSEIMPVDGVFIYVGLVPLTK 247
QY 247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVDRKGLRQIVTATGDSIAQAQSAEYIE 306
Db 248 AFLSLGIDEGYIVTDEMTNLPGIFAAAGDVRAKSLRQIVTATGDSGLAGNAQKYVE 307
QY 307 HLND 310
Db 308 ELKE 311
RESULT 5
TRXB LISMO
ID TRXB LISMO STANDARD; PRT; 319 AA.
AC O32823;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN TRXB OR LMO2478.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=EGD / Serovar 1/2a;
RA Borovok I., Mislovati M., Cohen G., Aharonowitz Y.;
RT "Isolation, cloning and characterization of the Listeria monocytogenes
RT thioredoxin reductase gene, trxB.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rueniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Kurapkat G.,
RA Jones L.-M., Kaerst U., Kuhn M., Kunst F., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC
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CC
CC EMBL; AF009622; AAB63804.1; -
CC EMBL; AL591983; CAD00556.1; -
CC FIR; AF1384; AF1384.
CC HSP; Q39243; LVDC.
CC ListList; LMO02478; -
CC InterPro; IPR000759; Adrndx_reductase.
CC InterPro; IPR001327; FAD_Pyr_redox.
CC InterPro; IPR001100; Pyr_redox.
CC InterPro; IPR008255; Pyr_redox2_AS.

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DR	InterPro; IPR000103; Pyridine_redox_2.
DR	InterPro; IPR003042; Rng_mnoxygenase.
DR	InterPro; IPR005982; Thio-redox_reduct.
DR	Pfam; PF00070; pyr_redox_1.
DR	PRINTS; PR00419; ADXRDTASE.
DR	PRINTS; PR00368; FADPNR.
DR	PRINTS; PR00411; PNDRTTASEI.
DR	PRINTS; PR00469; PNDRTTASEII.
DR	TIGRFAMS; TIGR01292; TRX_reduct; 1.
DR	KW Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW	Complete proteome.
FT NP_BIND	37 44 FAD (ADP PART) (BY SIMILARITY).
FT DISULFID	136 139 REDOX-ACTIVE (BY SIMILARITY).
FT NP_BIND	279 288 FAD (FLAVIN PART) (BY SIMILARITY).
SQ SEQUENCE	319 AA; 34173 MW; 8D42F36970611979 CRC64;
Query Match 63.4%; Score 1054; DB 1; Length 319;	
Best Local Similarity 65.5%; Pred. No. 4.3e-69;	
Matches 199; Conservative 43; Mismatches 62; Indels 0; Gaps 0;	
QY	7 FDIAIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTVEENFPFGEMITGPDLST 66
Db	8 YDVIIAGPAGMTAALVTTSRADLTLMERGVPGQMVNTAEVNYPFDSILGPLSD 67
QY	67 KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFNGNKELTAKAVIATGAEYKKIGVPGEQ 126
Db	68 KMLSGAKFGAEAYAGDIKEVVVDGKEFKTVTAGSKTYKARAIIITATGAHRKLGAAGEE 127
QY	127 LGRGVSYCAVDCGDAFFKNKLFVVGGSVAEEGTFTTKADKVTIVHRRDELRAQRIL 186
Db	128 LSGRGVSYCAVDCGDAFFKNRELIVVGGDSAVEEGTYLTRADKVTIVHRRDKLRAQQIL 187
QY	187 QDRAFKNKDIFIWSHTTKSINEKDGKGVSLTSTKGSEETHEADGVFIYGMKPLTA 246
Db	188 QDRAFKKEKDFIWNSTVEEVGDKKVTGAKLVSTVDGSESIMPVGVFIYGLVLPTK 247
QY	247 PFDLGHTNDVGYITVKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSTAQAAYIE 306
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QY	307 HLND 310
Db	308 ELKE 311
RESULT 6	
ID	TRXB_EUBAC STANDARD; PRT; 315 AA.
AC	PS0971;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DE	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN	TXRB.
OS	Eubacterium acidaminophilum.
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
OC	Eubacterium.
NCBI_TaxID=1731;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=D5M2 3953;
RA	MEDLINE=94039119; PubMed=8223622;
RX	Luebbens M., Andreesen J.R.;
RT	"Components of glycine reductase from Eubacterium acidaminophilum.
RT	Cloning, sequencing and identification of the genes for thioredoxin
RT	reductase, thioredoxin and selenoprotein PA.";
RN	Eur. J. Biochem. 217:791-798 (1993).
RP	[2]
RP	REVISION TO 275.
RA	Andreesen J.R.;
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

DR	InterPro; IPR000103; Pyridine_redox_2.
DR	InterPro; IPR003042; Rng_mnoxygenase.
DR	InterPro; IPR005982; Thio-redox_reduct.
DR	Pfam; PF00070; pyr_redox_1.
DR	PRINTS; PR00419; ADXRDTASEI.
DR	PRINTS; PR00368; FADPNR.
DR	PRINTS; PR00411; PNDRTTASEII.
DR	PRINTS; PR00469; PNDRTTASEII.
DR	TIGRFAMS; TIGR01292; TRX_reduct; 1.
DR	PROSITE; PS00573; PYRIDINE_REDUX_2; 1.
KW	Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW	Complete proteome.
FT	NP_BIND 37 44 FAD (ADP PART) (BY SIMILARITY).
FT	DISULFID 136 139 REDOX-ACTIVE (BY SIMILARITY).
FT	NP_BIND 279 288 FAD (FLAVIN PART) (BY SIMILARITY).
SQ	SEQUENCE 319 AA; 34173 MW; 8D42F36970611979 CRC64;
Query Match 63.4%; Score 1054; DB 1; Length 319;	
Best Local Similarity 65.5%; Pred. No. 4.3e-69;	
Matches 199; Conservative 43; Mismatches 62; Indels 0; Gaps 0;	
QY	7 FDIAIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPFGEMITGPDLST 66
Db	8 YDVIIAGPAGMTAALVTTSRADLTLMERGVPGQMVNTAEVNYPFDSILGPLSD 67
QY	67 KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFNGNKELTAKAVIATGAEYKKIGVPGEQ 126
Db	68 KMLSGAKFGAEAYAGDIKEVVVDGKEFTVTAGSKTYKARAIIITATGAHRKLGAAGEE 127
QY	127 LGRGVSYCAVDCGDAFFKNKLFVVGGSVAVEEGTTFKADKVTIVHRRDELRAQRIL 186
Db	128 LSGRGVSYCAVDCGDAFFKNRELIVVGGSVAVEEGTLYTRADKVTIVHRRDKLRAQQIL 187
QY	187 QDRAFKNKDIDFIWSHTTKSINEXDCKVGVTLTSTDGSEETHEADGVFIYGMKPLTA 246
Db	188 QDRAFKKVDIFWNSTVEEVGVGKVTGAKLVSTVDGSESIMPVGVFIYGLVLPTK 247
QY	247 PFDLGHTNDVGYITVKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGSTAQAAYIE 306
Db	248 AFLNLGITDDEGYITVDEMFNLPGLFAAGDVRKSLRQIVTATGSGLAGQNAKYVE 307
QY	307 HIND 310
Db	308 ELKE 311
RESULT 6	
ID	TXRB_EUBAC STANDARD; PRT; 315 AA.
AC	PS0971;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN	TXRB.
OS	Eubacterium acidaminophilum.
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
OC	Eubacterium.
NCBI_TaxID=1731;	
RP	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=D5M2 3953;
RX	MEDLINE=94039119; PubMed=8223622;
RA	Luebberts M., Andreesen J.R.;
RT	"Components of glycine reductase from Eubacterium acidaminophilum.
RT	Cloning, sequencing and identification of the genes for thioredoxin
RT	reductase, thioredoxin and selenoprotein PA.";
RN	Eur. J. Biochem. 217:791-798 (1993).
RP	REVISION TO 275.
RP	Andreesen J.R.;
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

RN	RP	SEQUENCE OF 1-54.
RX	RA	MEDLINE=89155433; PubMed=2537814;
RT	RT	Freundenberg W., Dietrichs D., Lebertz H., Andreesen J.R.;
RT	RT	"Isolation of an atypically small lipamide dehydrogenase involved in
RL	RL	the glycine decarboxylase complex from Eubacterium acidaminophilum.";
CC	-!	J. Bacteriol. 171:1346-1354 (1989).
CC	-!	CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC	-!	+ NADPH.
CC	-!	COFACTOR: Binds 1 FAD per subunit (By similarity).
CC	-!	SUBUNIT: Homodimer (By similarity).
CC	-!	SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC	-!	MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC	-!	SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC	-!	oxidoreductase family.

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CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; LO4500; AAB93303.1; --	
DR	HSSP; P09625; LTDE.	
DR	InterPro; IPR000759; Adrndx_reductase.	
DR	InterPro; IPR001327; FAD_pyr_redox.	
DR	InterPro; IPR001100; Pyr_redox.	
DR	InterPro; IPR008255; Pyr_redox2_AS.	
DR	InterPro; IPR000103; Pyridine_redox_2.	
DR	InterPro; IPR005982; Thioredox_reduct.	
DR	Pfam; PF00070; pyr_redox; 1.	
DR	PRINTS; PR00419; ADXRDTASEI.	
DR	PRINTS; PR00368; FADPNR.	
DR	PRINTS; PR00411; PNDRTTASEII.	
DR	PRINTS; PR00469; PNDRTTASEII.	
DR	TIGRFAMS; TIGR01292; TRX_reduct; 1.	
DR	PROSITE; PS00573; PYRIDINE_REDUX_2; 1.	
KW	Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.	
FT	NP_BIND 34 41 FAD (ADP PART) (BY SIMILARITY).	
FT	DISULFID 134 137 REDOX-ACTIVE (BY SIMILARITY).	
FT	NP_BIND 282 291 FAD (FLAVIN PART) (BY SIMILARITY).	
SQ	SEQUENCE 315 AA; 34033 MW; 145B0EABB2B8A7FA CRC64;	
Query Match 43.7%; Score 726; DB 1; Length 315;		
Best Local Similarity 49.8%; Pred. No. 2e-45;		
Matches 153; Conservative 50; Mismatches 96; Indels 8; Gaps 3;		
QY	7 FDIAIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPFG-FEWITGPDLS 65	
Db	5 YDLAIIGSPAGLAALYGARAKMTIMEGQKVGQIVTHEVANYPGSVREATGPSLI 64	
QY	66 TKMFEHAKFGAVYQYGDIKSVEDKGEYKVINFNGNKELTAKAVIATGAEYKKIGVPGEQ 125	
Db	65 ERMEQANEFGAEKVMKDVIDLDGKIWKGERAEYKAKSVILTGAAPPLAGCPGEQ 124	
QY	126 ELGGRGVSYCAVDCGDAFFKNKLFVVGGSVAVEEGTTTFADKVTIVHRRDELRAORI 185	
Db	125 ELTGKGVSYCATCDADFEDMEVFVVGGDTAVEEAMYLAKFARKVTIVHRRDELRAAKS 184	
QY	186 LDRAFKNKDIDFIWSHTTKSINEXDCKVGVTLTSTDGSEETHEADGVFIYI 239	
Db	185 IOEKAFKPKLDFWMNSALEEI-KGDGIVESAVFNKLVGTGETTEVFANEEDGTGFIFVI 243	
QY	240 GMKPETAPEKDLGINTDVGIVTVKDDMTTSVPGIFAAGDVRDKGLRQIVTATGSGIAAQ 299	
Db	244 GYIPKSDVFKGIITLDDAGYIITDNMKTNVEGVFAAGDIRKVSIRQVVTACADGATAAT 303	
QY	300 SAAEYIE 306	
Db	304 QAEKYVE 310	

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126 ELGGRGVSVCAGCAGFAFFKFKRLFVIGGDSABVEGTTTTPADKVTIVHRRDELRAORI 185
125 ELTGKGVSVYCATCDADFFEDMEVFVIGGDTAVEEAMFLTFARKVTIVHRRDELRAAKS 184
186 IQDRAFKNDKIDFWSHHTTKSINEKDKGVSVTLTSTKDG-----SSETHEADGVFIYI 239
185 IQEKAFFKNEKLNFMWNTVIEEI-KGDGIVESAVFKNRRTGETVTEFVAPEEDTGFIFVFI 243
240 GNMKPLTAPPKDLGITNDVGYIVTKDDMTTSVPGIFAAAGDVRDKGLRQIVTATGDSIAAO 299
244 GYDPSALVEGKLELDETYIPTDDNMKNVGVFAAGDIRVKLSRFQVVTATADGAIAAV 303
300 SAAEYIEHL 308
304 QAEKYEEL 312

RESULT 7
TXRB_CLOLI STANDARD; PRT; 315 AA.
ID TXRB_CLOLI
AC P52213;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN TXRB.
OS Clostridium litoreale (Bacterium W6).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96096738; PubMed=8529640;
RA Kreimer S., Andreesen J.R.;
RT "Glycine reductase of Clostridium litoreale. Cloning, sequencing, and
RT molecular analysis of the grdAB operon that contains two in-frame TGA
RT codons for selenium incorporation.";
RL Eur. J. Biochem. 234:192-199(1995).
CC -|- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -|- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -|- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC
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CC EMBL; U24268; AAC43575.1; -.
CC PIR; S63990; S63990.
CC HSSP; Q39243; 1VDC.
CC InterPro; IPR000759; Adrndx_reductase.
CC InterPro; IPR001327; FAD_pyr_redox.
CC InterPro; IPR001100; Pyr_redox.
CC InterPro; IPR008255; Pyr_redox2_AS.
CC InterPro; IPR000103; Pyridine_redox_2.
CC InterPro; IPR005982; Thioredox_reduct.
CC Pfam; PF00070; Pyr_redox; 1.
CC PRINTS; PR00419; ADXRDTASE.
CC PRINTS; PR00368; FADPNR.
CC PRINTS; PR00411; PNDRDTASEI.
CC PRINTS; PR00469; PNDRDTASEII.
CC TIGRfams; TIGR01292; TRX_reduct_1.
CC PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
KW Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.
FT NP BIND 34 41 FAD (ADP PART) (BY SIMILARITY).
FT DIISULFID 134 137 REDOX-ACTIVE (BY SIMILARITY).
FT NP BIND 282 291 FAD (FLAVIN PART) (BY SIMILARITY).
SQ SEQUENCE 315 AA; 33946 MW; 2CA55D36E579B2EF CRC64;

Query Match 42.5%; Score 706; DB 1; Length 315;
Best Local Similarity 48.5%; Pred. No. 5.6e-44;
Matches 150; Conservative 53; Mismatches 98; Indels 8; Gaps 3;

QY 7 FDIATIGAGPAGTAAVYASRANLKTVMTERGIPGGQMANTEEVENFPG-FEMITGPDLS 65
DB 5 YDIATIGSGPAGLAALYGARAKCKTLLLEGKMKVGGQIVITHEVANYPGSVPEATGPSLI 64
QY 66 TKMFEHAKFKGAVYQYQYCDIKSVDRDKGEYKVINFGNKKELTAKAVIITATGAIEYKKGIVPGSQ 125
DB 65 GRMEEQVEFGAERVMDNIVDFDTDKIKVLKGAKEGYKAKAVIVATGASPKLAGCPGEX 124

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[illegible]

Db 62 WLMQMYNAQKNVGTETVSDVYKVDLSKRPFKVTGAGNEYDAESIICCTGABAKWLG 121
 QY 122 PGEQELGGRGVSVCACDGAFFKKNRFLVIGGGDSAVEEGFTTKFADKVTIVHRRDEL 181
 Db 122 ASEQKFRGFGVSACATCDGFFKQNEIVVGGGSAVEEALYLNHANKVTIVHRRDSFR 181
 QY 182 AQRILQDRAFKNDKIDFWSHTTSKINEKDGKVGSG---VLTSTKDGSEETHE-----AD 233
 Db 182 AEKILQDLRFKNSKISVIWDHVVDEI-----VGSNPKPSVTGKYIQNVHTKELISLNC 235
 QY 234 GVFIYIGMKPLTAFPKDLGINTDVGIVYTKDDMT-TSVPGLFAAGDVRDKGLRQIVTATG 292
 Db 236 GVFIAGHANVGLTGTQIVMDDNYIITKSGTTRTSVEGVFAAGDVQDKIYRQAVTAAG 295
 QY 293 DGSIAAQAAYEI 305
 Db 296 TGCMAALEAEKEL 308

RESULT 12

TRXB MYCTU STANDARD; PRT; 335 AA.
 AC P52214; O53592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Thioresoxin reductase (EC 1.8.1.9) (TRXR) (TR).
 GN TRXB OR RV3913 OR MT4032 OR MTV028.04.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wiles B., Philip W., Drijfhout J.W., Offringa R.,
 RA Ottenhoff T.H.M.;
 RA "Sequence analysis and functional characterization of thioresoxin and
 RT thioresoxin reductase of Mycobacterium tuberculosis."
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekai F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Ruster S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sutton J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RL complete genome sequence."
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RX MEDLINE=22206494; PubMed=12218036;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 RL laboratory strains."
 RN J. Bacteriol. 184:5479-5490(2002).
 CC -!- CATALYTIC ACTIVITY: Thioresoxin + NADP(+) = thioresoxin disulfide
 CC + NADPH.
 CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
 CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide

oxido-reductase family.

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CC ENBL; X95798; CAA65070.1; --
 CC ENBL; AL021426; CAA16226.1; --
 CC ENBL; AE007194; AAK48397.1; --
 CC PIR; A70851; A70851.
 CC HSSP; Q39243; 1VDC.
 CC TIGR; MT4032; --
 CC TubercuList; RV3913; --
 DR InterPro; IPR000759; Admndx_reductase.
 DR InterPro; IPR001327; FAD_pyr_redox.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR008255; Pyr_redox2.
 DR InterPro; IPR000103; Pyridine_redox2.
 DR InterPro; IPR005982; Thioresoxin_redox.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEII.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGRFAMs; TIGR01292; TRX_redox; 1.
 DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
 KW Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
 KW Complete proteome.
 FT NP_BIND 44 51
 FT DISULFID 145 148
 FT NP_BIND 288 297
 FT CONFLICT 125 125
 FT CONFLICT 215 215
 FT CONFLICT 228 228
 SQ SEQUENCE 335 AA; 35643 MW; 3D0DD581E6C187E2 CRC64;
 Query Match 38.5%; Score 639.5; DB 1; Length 335;
 Best Local Similarity 46.4%; Pred. No. 3.9e-39;
 Matches 141; Conservative 54; Mismatches 104; Indels 5; Gaps 5;

QY 8 DIAIAGAPAGMTAAVYASRANLKTWIERGIPGGOMANTEVEVFPGFEM-ITGPDILT 66
 Db 16 DVIVIGSGPAGYTAALYARQAQLAPLVFEGTSFGALMTTDDVENYPGFRNGITGPELMD 75
 QY 67 KMFHAKKFGAVYQVDIKSVEDKGEYK-VINFGNKELTAKAVIATGAAYKKGVPGEQ 125
 Db 76 EMREQALFQADLRMEDVESVSLHGPLKSVVTADGQTHRARAVILAMGAARYLQVPEQ 135
 QY 126 ELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGFTTKFADKVTIVHRRDELRAQR 185
 Db 136 ELLGRGVSSCATCGFFFRDQDIAGVIGGDSAMEEATFLTRFARSVTLVHRRDFRASK 195
 QY 186 LQDRAFNKDKIDFIWSHTTSKINEKDGKVGSVTUTSTKDGSEETHEADGVFIYGMKPLT 245
 Db 196 MLDSARNNDKIRFLTNHTVAV-DGDTTVGLRVDRDNTGAEITPLVTGVFAVIGHEPRS 254
 QY 246 APFKDLGITNDVGVITVKDDMT-TSVPGLFAAGDVRDKGLRQIVTATGDSIAAQAAYEI 304
 Db 255 GLVREADIVDPDGVYLVQGRTTSTSLPGVFAAGDLVDRTYRQAVTAAGSGCAAIDAERW 314
 QY 305 I-EH 307
 Db 315 LAEH 318

RESULT 13

TRXB MYCTU STANDARD; PRT; 458 AA.
 ID TRXB MYCTU
 AC P46843;

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DR InterPro; IPR005746; Thioredoxin.
DR Pfam; PF00070; PVI_redox; 1.
DR Pfam; PF00085; thioRed; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNRDRTASEI.
DR PRINTS; PR00469; PNRDRTASEII.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfam; TIGR01068; thioredoxin; 1.
DR TIGRfam; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR PROSITE; PS00573; PYRIDINE REDOX 2; 1.
DR Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
KW Electron transport; Complete proteome.
FT DOMAIN 1 321 THIOREDOXIN REDUCTASE.
FT DOMAIN 322 347 LINKER.
FT DOMAIN 348 458 THIOREDOXIN.
FT NP_BIND 41 48 FAD (ADP PART) (BY SIMILARITY).
FT DISULFID 142 145 REDOX-ACTIVE (BY SIMILARITY).
FT NP_BIND 285 294 FAD (FLAVIN PART) (BY SIMILARITY).
FT DISULFID 379 382 REDOX-ACTIVE (BY SIMILARITY).
SQ SEQUENCE 458 AA; 49046 MW; 84D367AB31899987 CRC64;

Query Match 38.1%; Score 632.5; DB 1; Length 458;
Best Local Similarity 45.3%; Pred. No. 1.8e-38;
Matches 140; Conservative 53; Mismatches 111; Indels 5; Gaps 5;

QY 8 DIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEVEVPPGFEM-ITGPDLSLT 66
Db 13 EVIVGSGPAGYTAALYAAQAQLTPLVFEGTSFGGALMTTEVENYVGFNGITGPELMD 72
QY 67 KMEFAHAKFGAVYQYGDIKSVEDKGEYK-VINFGNKELTAKAVIATGAAYKKIGVPEQ 125
Db 73 DMREQALRFGAELRTEDVESVLSRGPISVTVTAEGQYQARAVILAMGTSVRYLIQIFEQ 132
QY 126 ELGGRGVSYCAVCDGAFKFKRRLFVIGGGSAAVEEGFTTKFKADKVTIVVHRDELRAQRI 185
Db 133 ELLGRGVSACTCDGSPFRGQDIAVIGGGSAAVEEALFLTRFARSVTLVHRDRDEFRASKI 192
QY 186 LQPAFKNKIDFTWSHTTKSINEKDKGVSVTLTSTKDGSEETHEADGVFIYIGMKPLT 245
Db 193 MLGRARNNDKIKFITNHTVAVNGYTTVG-LRLNNTTGTETTLVTVGVFVAIGHPEPS 251
QY 246 APFRDLGITNDVGIVYTKDDMT-TSVPGIFAAGVRDKGLRQIVTATDGDGSIQAQSAEY 304
Db 252 SLVSDVDVDIDPDGYVLVKGRTTSTMDGVFAAGDLVDRTYRQAITAAGSGCAAIDAERW 311
QY 305 I-EHLNDOA 312
Db 312 LAEHAGSKA 320

RESULT 14
TRXB_STRCO STANDARD; PRT; 321 AA.
AC P52215;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Thioredoxin reductase (EC 1.8.1.9) (TRXR).
GN TRXB OR SCO3890 OR SCH24.12C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA MEDLINE=99014240; PubMed=9795152;
RX Gal-Mor O., Borovok I., Av-Gay Y., Cohen G., Aharonowitz Y.;
RT "Gene organization in the trxA/B-oriC region of the Streptomyces
RL coelicolor chromosome and comparison with other eubacteria.";
Gene 217:83-90 (1998).

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bifunctional thioredoxin reductase/thioredoxin [Includes: Thioredoxin
DE reductase (EC 1.8.1.9) (TRXR); Thioredoxin].
GN TRXB/A OR TRX OR ML2703.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97124199; PubMed=8969512;
RA Feihl H., de Rossi E., Salazar L., Cantoni R., Labo M., Riccardi G.,
RA Takiff H.E., Eiglmeyer K., Bergh S., Cole S.T.;
RT "Gene arrangement and organization in an approximately 76 kb fragment
RT encompassing the orfC region of the chromosome of Mycobacterium
RT leprae.";
RL Microbiol. 142:3147-3161 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96059638; PubMed=7476189;
RA Wieleb B., van Soelingen D., Holmgren A., Offringa R., Ottenhoff T.,
RA Thole J.;
RT "Unique gene organization of thioredoxin and thioredoxin reductase in
RT Mycobacterium leprae.";
RL Mol. Microbiol. 16:921-929 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011 (2001).
CC -1- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
CC + NADPH.
CC -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -1- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
CC oxidoreductase family.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -----
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CC EMBL; X87899; CA861150.1; -.
CC EMBL; AL583926; CAC32235.1; -.
CC F01; S77662; S77662.
CC HSP; P80579; 1QWU.
CC Leproma; ML2703; -.
CC InterPro; IPR000759; Adnrxn_reductase.
CC InterPro; IPR001327; FAD_PVI_redox.
CC InterPro; IPR001100; Pyr_redox.
CC InterPro; IPR008255; Pyr_redox2_AS.
CC InterPro; IPR000103; Pyridine_redox_2.
CC InterPro; IPR006662; Thiored.
CC InterPro; IPR006663; Thioredox_dom2.
CC InterPro; IPR005982; Thioredox_reduct.

```

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[2]
REVIEWS.
RC STRAIN=A3(2) / M145;
RA Aharonowitz Y.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
"Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- CATALYTIC ACTIVITY: Thioresdoxin + NADP(+) = thioresdoxin disulfide
+ NADPH.
CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
CC -!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
oxidoreductase family.
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EMBL; X92105; CAA63076.1; --
EMBL; X92104; CAA63075.1; --
EMBL; AJ007313; CAA07451.1; --
EMBL; AL939118; CAB42713.1; --
DR PIR; T36577; T36577.
DR PIR; T42062; T42062.
DR HSSP; Q39243; LVDC.
DR InterPro; IPR00759; Admndx_reductase.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR008255; Pyr_redox2_AS.
DR InterPro; IPR00103; Pyridine_redox_2.
DR InterPro; IPR005982; Thioresdox_reduct.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR PRINTS; PR00469; PNDRTASEII.
DR TIGRFAMs; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
DR Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
Complete proteome.
FF FT 0 0 BY SIMILARITY.
FF INIT-MET 33 41 FAD (ADP PART) (BY SIMILARITY).
FF NP BIND 30 138 REDOX-ACTIVE (BY SIMILARITY).
FF FT 278 287 FAD (FLAVIN PART) (BY SIMILARITY).
FF NP BIND 25 25 A -> R (IN REF. 1; CAA63075/CAA07451).
FF CONFLICT 72 73 ER -> DG (IN REF. 1; CAA63075/CAA07451).
FF CONFLICT 154 154 MISSING (IN REF. 1; CAA63075).
FF CONFLICT 233 233 G -> A (IN REF. 1; CAA63075).
FF CONFLICT 257 257 MISSING (IN REF. 1; CAA63075).
FF CONFLICT 299 299 V -> L (IN REF. 3).
FF CONFLICT 303 303 P -> R (IN REF. 3).
FF SEQUENCE 321 AB; 34024 MW; 3A829A566A8345AE CRC64;

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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:12:53 ; Search time 115 Seconds
(without alignments)
877.964 Million cell updates/sec

Title: US-09-825-212-1

Perfect score: 1662

Sequence: 1 MGTEIDIDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHH 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1582	95.2	311	2	054079	054079 staphylococ
2	1582	95.2	311	16	Q99VL2	Q99VL2 staphylococ
3	1487	89.5	291	2	Q9X07	Q9X07 staphylococ
4	1455	87.5	310	16	Q8CP8	Q8CP8 staphylococ
5	1173	70.6	318	16	Q81X56	Q81X56 bacillus an
6	1170	70.4	321	16	Q815J1	Q815J1 bacillus ce
7	1146	69.0	315	16	Q8CX98	Q8CX98 oceanobacil
8	1145.5	68.9	315	16	Q9K703	Q9K703 bacillus ha
9	943	56.7	312	16	Q88Y17	Q88Y17 lactobacill
10	940	56.6	304	16	Q83N8	Q83N8 enterococcu
11	899	54.1	305	16	Q8N2Y5	Q8N2Y5 streptococ
12	897	54.0	305	16	Q8K6D2	Q8K6D2 streptococ
13	882	53.1	304	16	Q8DVL7	Q8DVL7 streptococ
14	872	52.5	308	16	Q9CH02	Q9CH02 lactococcu
15	852.5	51.3	304	16	Q8E773	Q8E773 streptococ
16	852.5	51.3	304	16	Q8E1Q9	Q8E1Q9 streptococ

17	851	51.2	303	16	Q8DP78	Q8dp78 streptococ
18	849	51.1	303	16	Q97PY2	Q97py2 streptococ
19	815	49.0	310	2	Q93FC9	Q93fc9 lactobacill
20	753	45.3	314	2	Q9EV96	Q9ev96 clostridium
21	746	44.9	305	16	Q8R817	Q8r817 thermoanaer
22	741	44.6	308	16	Q8R8V8	Q8r8v8 thermoanaer
23	728.5	43.8	325	16	Q9RSY7	Q9rsy7 deinococcus
24	687	41.3	317	16	Q9WZ3	Q9wz3 thermotoga
25	682.5	41.1	311	16	Q8KE48	Q8ke48 chlorobium
26	671	40.4	308	16	Q97KP8	Q97kp8 clostridium
27	647.5	39.0	341	16	Q8G6J1	Q8g6j1 bifidobacte
28	645.5	38.8	345	17	Q9VQ08	Q9vq08 pyrococcus
29	643.5	38.7	336	17	Q50134	Q50134 pyrococcus
30	641.5	38.6	336	2	Q93AQ4	Q93aq4 mycobacteri
31	639.5	38.4	356	17	Q8U108	Q8u108 pyrococcus
32	638.5	38.4	305	17	Q8PUI1	Q8puil methanosarc
33	635.5	38.2	335	16	Q7TVC8	Q7tvc8 mycobacteri
34	634	38.1	313	16	Q8FSW1	Q8fsw1 corynebacte
35	629.5	37.9	326	16	Q8RIS2	Q8ris2 streptomyce
36	626	37.7	315	16	Q897A0	Q897a0 clostridium
37	625	37.6	317	16	Q8NLS9	Q8ntl59 corynebacte
38	622.5	37.5	315	17	Q8TR16	Q8tr16 methanosarc
39	613.5	36.9	323	16	Q82FE8	Q82fe8 streptomyce
40	606	36.5	320	16	Q8EUJ3	Q8eu3 mycoplasma
41	604	36.3	318	2	Q9X5F7	Q9x5f7 zymomonas m
42	599.5	36.1	303	17	Q26804	Q26804 methanobact
43	596.5	35.9	556	16	Q8XMA7	Q8xma7 clostridium
44	594.5	35.8	333	10	Q84W20	Q84w20 arabidopsis
45	592.5	35.6	453	16	Q8DHM2	Q8dhm2 synechococ

ALIGNMENTS

RESULT 1

054079 PRELIMINARY; PRT; 311 AA.
AC Q54079; Q9RL89;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Thioredoxin reductase (EC 1.6.4.5) (Thioredoxine reductase).
GN TRXB
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Oxford;
RA Uziel O., Borovok I., Schreiber R., Aharonowitz Y., Cohen G.;
RT "Transcriptional analysis of the thioredoxin (trxB) and thioredoxin reductase (trxB) genes from Staphylococcus aureus";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Oxford;
RA Borovok I.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-RUSA277;
RX MEDLINE=20031141; PubMed=10566865;
RA de Lencastre H., Wu S.W., Pinho M.G., Ludovice A.M., Filipe S., Gardete S., Sobral R., Gill S., Chung M., Tomasz A.;
RT "Antibiotic resistance as a stress response: complete sequencing of a large number of chromosomal loci in Staphylococcus aureus strain COL that impact on the expression of resistance to methicillin";
RL Microb. Drug Resist. 5:163-175(1999).
DR EMBL; AJ223781; CAA11546.2; -
DR EMBL; Y18636; CAB60740.1; -
DR PIR; B89849; E89849.
DR HSSP; Q39243; 1VDC.
GO; GO:0005737; C:cytoplasm; IEA.

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MW2;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 CC !- COFACTOR: FAD (BY SIMILARITY).
 DR EMBL; AF003360; BAB56926.1; -;
 DR EMBL; AF003131; BAB1952.1; -;
 DR EMBL; AF004824; BAB94591.1; -;
 DR PIR; E89849; E89849.
 DR HSSP; Q39243; 1VDC.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR000759; Adrnx reductase.
 DR InterPro; IPR001327; FAD pyr redox.
 DR InterPro; IPR000103; Pyridine redox_2.
 DR InterPro; IPR001100; Pyr redox.
 DR InterPro; IPR008255; Pyr redox2 AS.
 DR InterPro; IPR005982; Thioredox_reduct.
 DR Pfam; PF00070; Pyr redox; 1.
 DR PRINTS; PR00419; ADXRTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGRFAMS; TIGR01292; TRX reduct; 1.
 DR PROSITE; PS00573; PYRIDINE REDOX 2; 1.
 DR FAD; Flavoprotein; Oxidoreductase; Complete proteome.
 KW FAD; Flavoprotein; Oxidoreductase; Complete proteome.
 SQ SEQUENCE 311 AA; 33616 MW; 1A337DE3736C9265 CRC64;

Query Match 95.2%; Score 1582; DB 16; Length 311;
 Best Local Similarity 99.4%; Pred. No. 2e-104;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TEIDFDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPPGFEMITGP 62
 Db 2 TEIDFDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPPGFEMITGP 61
 Qy 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKLTAQAVIIATGAETKIGVP 122
 Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKLTAQAVIIATGAETKIGVP 121
 Qy 123 GEELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGTFTKFAADKVTIVHRRDELRA 182
 Db 122 GEELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGTFTKFAADKVTIVHRRDELRA 181
 Qy 183 QRILQDRAFNKDKIDFVWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
 Db 182 QRILQDRAFNKDKIDFVWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGADVDRDKGLRQIVTATGDSIAAQSAA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGADVDRDKGLRQIVTATGDSIAAQSAA 301
 Qy 303 EYIEHLNDQA 312
 Db 302 EYIEHLNDQA 311
 RESULT 3
 Q9KX07
 ID Q9KX07 PRELIMINARY; PRT; 291 AA.

DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR000759; Adrnx reductase.
 DR InterPro; IPR001327; FAD pyr redox.
 DR InterPro; IPR00103; Pyridine redox_2.
 DR InterPro; IPR001100; Pyr redox.
 DR InterPro; IPR008255; Pyr redox2 AS.
 DR InterPro; IPR005982; Thioredox_reduct.
 DR Pfam; PF00070; Pyr redox; 1.
 DR PRINTS; PR00419; ADXRTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGRFAMS; TIGR01292; TRX reduct; 1.
 DR PROSITE; PS00573; PYRIDINE REDOX 2; 1.
 DR Oxidoreductase.
 KW Oxidoreductase.
 SQ SEQUENCE 311 AA; 33616 MW; 1A337DE3736C9265 CRC64;

Query Match 95.2%; Score 1582; DB 2; Length 311;
 Best Local Similarity 99.4%; Pred. No. 2e-104;
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TEIDFDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPPGFEMITGP 62
 Db 2 TEIDFDIATGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEVENPPGFEMITGP 61
 Qy 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKLTAQAVIIATGAETKIGVP 122
 Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKLTAQAVIIATGAETKIGVP 121
 Qy 123 GEELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGTFTKFAADKVTIVHRRDELRA 182
 Db 122 GEELGGRGVSYCAVCDGAFKFKRLFVIGGDSAVEEGTFTKFAADKVTIVHRRDELRA 181
 Qy 183 QRILQDRAFNKDKIDFVWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
 Db 182 QRILQDRAFNKDKIDFVWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 241
 Qy 243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGADVDRDKGLRQIVTATGDSIAAQSAA 302
 Db 242 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAGADVDRDKGLRQIVTATGDSIAAQSAA 301
 Qy 303 EYIEHLNDQA 312
 Db 302 EYIEHLNDQA 311
 RESULT 2
 Q99VL2
 ID Q99VL2 PRELIMINARY; PRT; 311 AA.
 AC Q99VL2;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Thioredoxine reductase.
 GN TRXB OR SAV0764 OR SA0719 OR MW0726.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=159878, 159879, 196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MW50, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

AC 09X07;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COL;
 RX MEDLINE=20031141; PubMed=10566865;
 RA de Lencastre H., Wu S.W., Pinho M.G., Ludovice A.M., Filipe S.,
 RA Gardner S., Sobral R., Gill S., Chung M., Tomasz A.;
 RT "Antibiotic resistance as a stress response: complete sequencing of a
 RT large number of chromosomal loci in Staphylococcus aureus strain COL
 RT that impact on the expression of resistance to methicillin.";
 RL Microb. Drug Resist. 5:163-175(1999).
 DR EMBL; Y14324; CAB82468.1; -;
 DR HSP; Q39243; 1VDC.
 DR GO; GO:0005737; Cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR001327; FAD_pyr_redux.
 DR InterPro; IPR00103; Pyridine_redux_2.
 DR InterPro; IPR008255; Pyr_redux.
 DR InterPro; IPR001100; Pyr_redux.
 DR TIGRfams; TIGR01292; TRX_redux; 1.
 DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 291 AA; 31640 MW; 3C700EE8752343CF CRC64;
 Query Match 89.5%; Score 1487; DB 2; Length 291;
 Best Local Similarity 99.3%; Pred. No. 1e-97;
 Matches 289; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 22 AVASRANLKTVMIERGIPGGQMANTEEVNFFGFMITGPDLSITKMFHAKKFGAVYQY 81
 Db 1 AVASRANLKTVMIERGIPGGQMANTEEVNFFGFMITGPDLSITKMFHAKKFGAVYQY 60
 QY 82 GDIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIGVPGQEELGGRGVSVCVDCGA 141
 Db 61 GDIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIGVPGQEELGGRGVSVCVDCGA 120
 QY 142 FFKNKLRFVIGGDSAVESGTTTFAKDKVTIVHRRDELRAQRILODRAPKNDKIDFIWS 201
 Db 121 FFKNKLRFVIGGDSAVESGTTTFAKDKVTIVHRRDELRAQRILODRAPKNDKIDFIWS 180
 QY 202 HTTKSINEKDGKVSVTLSITKDGSETHADGVFIYIGMKPLTAPFKDLGINTDVGIV 261
 Db 181 HTKLSINEKDGKVSVTLSITKDGSETHADGVFIYIGMKPLTAPFKDLGINTDVGIV 240
 QY 262 TKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQAAYIEHLNDQA 312
 Db 241 TKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQAAYIEHLNDQA 291
 RESULT 4
 Q8CPY8 PRELIMINARY; PRT; 310 AA.
 AC Q8CPY8;
 DT 01-NAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Thioredoxine reductase.
 GN SE0547.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016745; AAC04144.1; -;
 DR GO; GO:0005737; Cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
 DR InterPro; IPR000759; Adrndx_reductase.
 DR InterPro; IPR001327; FAD_pyr_redux.
 DR InterPro; IPR00103; Pyridine_redux_2.
 DR InterPro; IPR001100; Pyr_redux.
 DR InterPro; IPR008255; Pyr_redux2_AS.
 DR InterPro; IPR005982; Thioredux_reduct.
 DR Pfam; PF00070; Pyr_redux; 1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 DR TIGRfams; TIGR01292; TRX_redux; 1.
 DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 310 AA; 33544 MW; D5D6853667137D8B CRC64;
 Query Match 87.5%; Score 1455; DB 16; Length 310;
 Best Local Similarity 90.3%; Pred. No. 2.1e-95;
 Matches 278; Conservative 17; Mismatches 13; Indels 0; Gaps 0;
 QY 3 TEIDFIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNFFGFMITGP 62
 Db 2 TEVDFVAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVNFFGFMITGP 61
 QY 63 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIGVP 122
 Db 62 DLSTKMFHAKKFGAVYQYGDIKSVEDKGEYKVFNGKELTAKAVIATGAAYKKIGVP 121
 QY 123 GEQELGGRGVSVCVDCGAFFKNKRLFVIGGDSAVEEGTFTTKPADKVTIVHRRDELRA 182
 Db 122 GEQELGGRGVSVCVDCGAFFKNKRLFVIGGDSAVEEGTFTTKPADKVTIVHRRDELRA 181
 QY 183 QRILQDRAPKNDKIDFIWSHTTKSINEKDGKVSVTLSITKDGSETHADGVFIYIGMK 242
 Db 182 QNIIQERAFKNDKIDFIWSHTTKSINEKDGKVSVTLSITKDGSETHADGVFIYIGMK 241
 QY 243 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQA 302
 Db 242 PLTAPFKDLGINTDVGIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQA 301
 QY 303 EYIEHLND 310
 Db 302 DYITELKD 309
 RESULT 5
 Q8IX56 PRELIMINARY; PRT; 318 AA.
 AC Q8IX56;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Thioredoxin reductase.
 GN TRXB OR BA5387.
 OS Bacillus anthracis (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=198094;

ID	Q8CX98	PRELIMINARY;	PRT;	315 AA.
AC	Q8CX98;			
DT	01-MAR-2003 (TReMBLrel. 23, Created)			
DT	01-MAR-2003 (TReMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)			
DE	Thioredoxin reductase (NADPH) (General stress protein)			
DE	(EC 1.6.4.5).			
GN	OB2469.			
OS	Oceanobacillus ihewensis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.			
OX	NCBI_TaxID=182710;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-HT831 / DSM 14371 / JCM 11309;			
RA	MEDLINE=2220767; PubMed=12235376;			
RA	Takami H., Takaki Y., Uchiyama I.;			
RT	"Genome sequence of Oceanobacillus ihewensis isolated from the Ihaya			
RT	ridge and its unexpected adaptive capabilities to extreme			
RT	environments.";			
RL	Nucleic Acids Res. 30:3927-3935 (2002).			
DR	EMBL; AP004601; BAC14425.1;			
DR	GO; GO:0005737; C:cytoplasm; IEA.			
DR	GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.			
DR	GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.			
DR	GO; GO:0006118; P:electron transport; IEA.			
DR	GO; GO:0019430; P:removal of superoxide radicals; IEA.			
DR	InterPro; IPR000759; Adrxnx reductase.			
DR	InterPro; IPR001327; FAD pyr redox.			
DR	InterPro; IPR000103; Pyridine_redox_2.			
DR	InterPro; IPR001100; Pyr_redox.			
DR	InterPro; IPR008255; Pyr_redox2_AS.			
DR	InterPro; IPR003042; Rng_mnoxigenase.			
DR	InterPro; IPR005982; ThioRedox_reduct.			
DR	Pfam; PF00070; Pyr_redox; 1.			
DR	PRINTS; PR00419; ADXRDASE.			
DR	PRINTS; PR00368; FADPNR.			
DR	PRINTS; PR00411; ENDRDTASE1.			
DR	PRINTS; PR00469; ENDRDTASE11.			
DR	PRINTS; PR00420; RINGMNOXGNASE.			
DR	TIGRFAMS; TIGR01292; TRX reduct; 1.			
DR	PROSITE; PS00573; PYRIDINE REDOX_2; 1.			
KW	Oxidoreductase; Complete Proteome.			
SQ	SEQUENCE 315 AA; 34337 MW; 6F0ED957848374F1 CRC64;			
Query Match 69.0%; Score 1146; DB 16; Length 315;				
Best Local Similarity 69.1%; Pred. No. 1.9e-73;				
Matches 217; Conservative 39; Mismatches 58; Indels 0; Gaps 0;				
QY	1	MCETIDFDIAIAGAPAGMTAAVYASRANIKTMIERGPGQVANTVEENFEGFEMIT	60	
Db	1	MSBEKMYDVIAGAPAGMTAAVYASRANLDTMLERGIPGGQVANTDEVENYEGFDNII	60	
QY	61	GPDLSTKMFPHAKFGAVYGYDGIKSVEDKGEYKVINFGNKELTAKAVIIATGAYKKIG	120	
Db	61	GPDLSNKMFPHAKFGAVAYGDIKEVEDHGEYKLIKAGSKYYTYRSLIIATGAQYKKLG	120	
QY	121	VPEQELGGRGVSVCVDCGAGFFKNKELFVIGGSDSAVEEGTFTTKFADKVTIVHREDEL	180	
Db	121	IEGEALSGRGVSVCVDCGAGFFKNRLVVIIGGDSAVEEGIYLTRFANKVTIVHRDNL	180	
QY	181	RAGRIILQDRAFKNDKIDDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYG	240	
Db	181	RAGRIILQDRAFDNEKIDFIDWTVAETINGTDGVSSVTLKNTKTNVWNFDASGVFIYG	240	
QY	241	MKELTAPFDGLGTNDVGIVTLTKDDMTTSVPG;FAAGDVDPDKGLRQIVTATGSGSIAAQS	300	
Db	241	MVPLNQAFSLGINTNEGVIATNENMETSPGIFAAGDIRDKELRQIVTATGSGSIAAEA	300	
QY	301	AABYIEHLNDQARS 314		
Db	301	AIKYVEDLEKIKS 314		

QY 307 HLNDQARS 314
DB 305 ALGDKVNN 312

RESULT 10
Q835N8 PRELIMINARY; PRT; 304 AA.

AC Q835N8;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Thioridoxin reductase.
GN TRXB OR EF1338.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
[1]
SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.K., Heidelberg J.P.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Madupu R., Nelson W.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Shetty J., Khouri H.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Fraser C.M.,
Uterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RA "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
EMBL; AE016951; AAC01129.1; -.
TIGR; EF1338; -.
DR GO: 0005737; C:cytoplasm; IEA.
DR GO: 0015036; F:disulfide oxidoreductase activity; IEA.
DR GO: 0004791; F:thioridoxin-disulfide reductase activity; IEA.
DR GO: 0006118; P:electron transport; IEA.
DR GO: 0019430; P:removal of superoxide radicals; IEA.
DR InterPro: IPR000759; Adrndx reductase.
DR InterPro: IPR001327; FAD pyr reduct.
DR InterPro: IPR001103; Pyridine reduct.
DR InterPro: IPR008255; Pyr reduct2 AS.
DR InterPro: IPR005982; Thioridox reduct.
DR Pfam: PF00070; Pyr reduct; 1.
DR PRINTS: PR00419; ADXDTASE.
DR PRINTS: PR00368; FADPNR.
DR PRINTS: PR00411; PNDRTASEII.
DR PRINTS: PR00469; PNDRTASEII.
DR PRODOM: PD000139; FAD pyr reduct; 1.
DR TIGRFAMS: TIGR01292; TRX reduct; 1.
DR PROSITE: PS00573; PYRIDINE_REDOX_2; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 304 AA; 33240 MW; F08B31A3E28628EE CRC64;

Query Match 56.6%; Score 940; DB 16; Length 304;
Best Local Similarity 58.9%; Pred. No. 7.7e-59;
Matches 178; Conservative 42; Mismatches 82; Indels 0; Gaps 0;

QY 7 FDIAIIGAGPAGTAAYASRANLKTVMIERGIPGGQVANTTEVENFPGFEMITGPDIST 66
DB 5 YDVIIIGAGPAGTAAYASRANLKTVMIERGIPGGQVANTTEVENFPGFEMITGPDIST 61
QY 67 KMFEHAKFGAVYQGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAAYKKIGVPGQE 126
DB 62 KMYENVEKFTGNTAAGVGVGIEDHGSYKEVICDDKSYEAKAVIATGCEHRLKGVKGE 121
QY 127 LGGRGVSYCAVCDGAPFFKPKRLFTVIGGSDSAVEEGTFTTKADKVTIVHRRDLRAORIL 186
DB 122 FAGRGVSYCAVCDGAPFFKPKRLFTVIGGSDSAVEEGTFTTKADKVTIVHRRDLRAORIL 181
QY 187 QDRAFNKIDFIWGHHTKTSINEKDGKGSVTLTSTKGSSEETHEADGVFIYGMKPLTA 246

QY 300 SAAEYIEHLNDQARS 314
DB 301 NVQHYIEELAERKVN 315

RESULT 9
Q88YJ7 PRELIMINARY; PRT; 312 AA.

AC Q88YJ7;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Thioridoxin reductase (NADPH) (EC 1.6.4.5).
GN TRXB1 OR LP 0761.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
NCBI_TaxID=1590;
[1]
SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kuijpers O.P., Leer K., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Siezen R.J.;
RA "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
EMBL; AL935254; CA063354.1; -.
DR GO: 0015036; F:disulfide oxidoreductase activity; IEA.
DR GO: 0006118; P:electron transport; IEA.
DR InterPro: IPR000759; Adrndx reductase.
DR InterPro: IPR001327; FAD pyr reduct.
DR InterPro: IPR000205; NADH.
DR InterPro: IPR000103; Pyridine reduct.
DR InterPro: IPR001100; Pyr reduct.
DR InterPro: IPR008255; Pyr reduct2 AS.
DR InterPro: IPR003042; Rng mnoxigenase.
DR Pfam: PF00070; Pyr reduct; 1.
DR PRINTS: PR00419; ADXDTASE.
DR PRINTS: PR00368; FADPNR.
DR PRINTS: PR00411; PNDRTASEII.
DR PRINTS: PR00469; PNDRTASEII.
DR PRINTS: PR00420; RINGMOXGNASE.
DR PROSITE: PS00573; PYRIDINE_REDOX_2; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 312 AA; 33455 MW; BF013DD361ED8343 CRC64;

Query Match 56.7%; Score 943; DB 16; Length 312;
Best Local Similarity 55.5%; Pred. No. 4.9e-59;
Matches 171; Conservative 54; Mismatches 83; Indels 0; Gaps 0;

QY 7 FDIAIIGAGPAGTAAYASRANLKTVMIERGIPGGQVANTTEVENFPGFEMITGPDIST 66
DB 5 YDVIIIGAGPAGTAAYASRANLKTVMIERGIPGGQVANTTEVENFPGFEMITGPDIST 64
QY 67 KMFEHAKFGAVYQGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAAYKKIGVPGQE 126
DB 65 DMYESATQGEAYAGSVESVEDRQDKVITVTDSTFTFKALVIGTGEYKLVGTGDT 124
QY 127 LGGRGVSYCAVCDGAPFFKPKRLFTVIGGSDSAVEEGTFTTKADKVTIVHRRDLRAORIL 186
DB 125 YGGRGVSYCAVCDGAPFFKPKRLFTVIGGSDSAVEEGTFTTKADKVTIVHRRDLRAORIL 184
QY 187 QDRAFNKIDFIWGHHTKTSINEKDGKGSVTLTSTKGSSEETHEADGVFIYGMKPLTA 246
DB 185 QDRAFNKIDFIWGHHTKTSINEKDGKGSVTLTSTKGSSEETHEADGVFIYGMKPLTA 244
QY 247 PFKDLGITNDGVYIVTKDMWTISVPGIFAGGVDVRKGLRQIVTATGDGSIQAQSAAYIE 306
DB 245 PFSNLGITDENGWIEIHNHETKVPGLFAVGVDVRKGLRQIVTATGDGSIQAQSAAYIE 304

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Db      182 QDFAFANEKISFVWDTVVVEIVGNEMVTVGVKARNVKTDEIVSEIANGVFYIVGLDPLTE 241
Qy      247 PFKDLGINTDYGIVTVDKDDMTTSVPGIPAAAGDVDRKGLRQIVTATGDSIAAQAAYIE 306
Db      242 PFKAGITNEAGWLETQEMTKIPGVYALGDVREKILRQITTAAGGAGQVFNYYIE 301
Qy      307 HL 308
Db      302 EL 303

RESULT 11
Q8NZY5
ID Q8NZY5 PRELIMINARY; PRT; 305 AA.
AC Q8NZY5
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thioresoxin reductase.
DE Thioresoxin reductase.
GN TRXB OR SPYM18 1666.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gorpel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AB010078; AAL98210.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
DR InterPro; IPR000759; Adrnrx_reductase.
DR InterPro; IPR001327; FAD_pyr_redux.
DR InterPro; IPR000103; Pyridine_redux_2.
DR InterPro; IPR001100; Pyr_redux.
DR InterPro; IPR008255; Pyr_redux2_AS.
DR Pfam; PF00070; PYR_redux; 1.
DR PRINTS; PR00419; ADXRDTSASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR TIGRfams; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
KW Complete proteome.
SQ SEQUENCE 305 AA; 33444 MW; 527858AF746BFF9D CRC64;

Query Match 54.1%; Score 899; DB 16; Length 305;
Best Local Similarity 56.3%; Pred. No. 6.3e-56;
Matches 169; Conservative 49; Mismatches 82; Indels 0; Gaps 0;

Qy      7 FDIATIGAPAGMTAAVYASRANLTKVTMIERGIPGGOMANTEEVNFGFEMITGPDIST 66
Db      2 YDTLIIGSPAGMTAAVYASRANLTKVTMIERGIPGGOMANTEEVNFGFEMITGPDIST 61
Qy      67 KMFHAKFGAVYQVGTDKSVEDKGEYKVINFGNKELTAKAVIATGAEYKKIGVPGQEE 126
Db      62 KMYEPLKFNVENIYGVQKIENFGDYKCVLTEDASYEAKTVIATGAKYVGVPGSEY 121
Qy      127 LGGRGVSYCAVCDGAGFFKKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRL 186
Db      122 YTRGSVSYCAVCDGAGFFKKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRL 181

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Qy      187 QDFAKNDKIDFINSHTTKSINERKDGKGVSVTLSTKDGSEETHEADGVFIYIGMKPLTA 246
Db      182 QDFAFANDKVDIWDVSVVKEIQGNDIKVSNVLIENVKTGQVTDHAFGCVFIYIGMNPVIG 241
Qy      247 PFKDLGINTDYGIVTVDKDDMTTSVPGIPAAAGDVDRKGLRQIVTATGDSIAAQAAYIE 306
Db      242 MVKDLITDSEGWIITDDHMRITSPGIFAIGDVQRKDLRQITTAAGGAGTAAQGVVHYLE 301

RESULT 12
Q8K6D2
ID Q8K6D2 PRELIMINARY; PRT; 305 AA.
AC Q8K6D2
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative thioredoxin reductase (putative NADH oxidase/alkyl
DE hydroperoxidase reductase).
GN NOX.2 OR SPYM3 1395 OR SPS0467.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014163; AAM80002.1; -.
DR GO; GO:0005142; BAC63562.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
DR InterPro; IPR000759; Adrnrx_reductase.
DR InterPro; IPR001327; FAD_pyr_redux.
DR InterPro; IPR000103; Pyridine_redux_2.
DR InterPro; IPR001100; Pyr_redux.
DR InterPro; IPR008255; Pyr_redux2_AS.
DR Pfam; PF00070; PYR_redux; 1.
DR PRINTS; PR00419; ADXRDTSASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR TIGRfams; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
KW Hypothetical protein; Peroxidase; Complete proteome.
SQ SEQUENCE 305 AA; 33543 MW; 3F947A628769E8BB CRC64;

Query Match 54.0%; Score 897; DB 16; Length 305;
Best Local Similarity 56.3%; Pred. No. 8.7e-56;
Matches 169; Conservative 49; Mismatches 82; Indels 0; Gaps 0;

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QY	67	KMFEHAKFGAVYQYGD	IKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKGIVGPEOE	126
DB	62	KMHEPLEKFGVENLYGI	VTAVEDHGNFKVLTDDNSYETKTVIIATGAKHPLAVAGEET	121
QY	127	LGGRVSYCAVCDGAFF	KFKRFLVIGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL	186
DB	122	YNSRGVSYCAVCDGAFF	RQDILLVGGDSAVEEALFLTRFANKVTIVHRRDELRAQKVL	181
QY	187	QDRAFPNDKIDFIWSHT	TKSINEKDGKGVSVTLTSTKDGSEETHADGVFIYIMKPLTA	246
DB	182	QERAFANDKVDFTWDS	VWEIKGNLDKVTNVNDIENKVTGQVNNYAFGGVFIYVGLDPVSS	241
QY	247	PKDLGITNDVGIYTKD	DMTTSVPGIFAAGDVRDKGLRQIVTATGDSIAAQAAYEYI	305
DB	242	MVKELDITDEAGWIP	DDHMKTKVAGVFAIGDVRQKDLRQITTAUGDGAQAQYQYI	300

RESULT 14

Q9CH02

ID

Q9CH02

PRELIMINARY;

PRT;

308 AA.

AC

Q9CH02;

DT

01-JUN-2001

(TrEMBLrel. 17, Created)

DT

01-JUN-2001

(TrEMBLrel. 17, Last sequence update)

DT

01-OCT-2003

(TrEMBLrel. 25, Last annotation update)

DE

Thioredoxin reductase (EC 1.6.4.5).

GN

TRXB1 OR LL0940.

OS

Lactococcus lactis (subsp. lactis) (Streptococcus lactis).

OC

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.

OX

NCBI_TaxID=1360;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

STRAIN=IL1403;

RX

MEDLINE=21235186; PubMed=11337471;

RA

Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,

RA

Weissenbach J., Ehrlich S.D., Sorokin A.;

RT

"The complete genome sequence of the lactic acid bacterium Lactococcus

RT

lactis ssp. lactis IL1403."

RL

Genome Res. 11:731-753(2001).

CC

-!- COFACTOR: FAD (BY SIMILARITY).

DR

EMBL; AE006328; AAK05038.1; -.

DR

PIR; D86742; D86742.

DR

HSSP; Q39243; 1VDC.

DR

GO; GO:0005737; C:cytoplasm; IEA.

DR

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

DR

GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.

DR

GO; GO:0006118; P:electron transport; IEA.

DR

GO; GO:0019430; P:removal of superoxide radicals; IEA.

DR

InterPro; IPR000759; Adrxn_reductase.

DR

InterPro; IPR001327; FAD_pyr_redox.

DR

InterPro; IPR000103; Pyridine_redox_2.

DR

InterPro; IPR001100; Pyr_redox.

DR

InterPro; IPR008255; Pyr_redox2_AS.

DR

InterPro; IPR005982; Thioredox_reduct.

DR

Pfam; PF00070; pyr_redox; 1.

DR

PRINTS; PR00419; ADXRDTASE.

DR

PRINTS; PR00368; FADPNR.

DR

PRINTS; PR00411; PNDRDTASEI.

DR

PRINTS; PR00469; PNDRDTASEII.

DR

TIGRFAMs; TIGR01292; TRX_reduct; 1.

DR

PROSITE; PS00573; PYRIDINE_REDOX_2; 1.

KW

FAD; Flavoprotein; Oxidoreductase; Complete proteome.

SQ

SEQUENCE 308 AA; 33894 MW; 363397A925E48267 CRC64;

Query Match

52.5%;

Score 872;

DB 16;

Length 308;

Best Local Similarity

53.1%;

Pred. No. 5.3e-54;

Matches 163;

Conservative 54;

Mismatches 90;

Indels 0;

Gaps 0;

QY	3	TEIDFDIIAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP	62	
DB	2	TEKYDVVIISGPGAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP	61	
QY	63	DLSTKMFHAKFGAVYQYGD	IKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKGIVP	122

QY	7	FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST	66
DB	2	YDTLIISGPGAGMTAAVYAAARSNSVAIEQAGPGQMNNTFDIENYPGDHISGPELAM	61
QY	67	KMFEHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKGIVGPEOE	126
DB	62	KMFEPELEKFNVENIYGIQVKLENFGDYKCVLTEDASYEAKVTIIATGAKYFVLGVPGEY	121
QY	127	LGGRGVSYCAVCDGAFKKRFLVIGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL	186
DB	122	YTSRGVSYCAVCDGAFRRDQDLLVGGGDSAVEEAIYLTQFAKKVTIVHRRDQLRAQKIL	181
QY	187	QDRAFNKDKIDFTWSHTTKSINEKDGKGVSVTLTSTKDGSEETHADGVFIYIMKPLTA	246
DB	182	QDRAFANDKVDFTWDSVWEIKGNLDIKSVNLLENVKTGQVTHAFGGVFIYVGNPNPTD	241
QY	247	PFKOLGITNDVGIYTKDDMTTSVPGIFAAGVDVRDKGLRQIVTATGDSIAAQSAAYEIE	306
DB	242	MVKDLEITDOEGMIITDDHMYTSIPGIFAIGDVRQKDLRQITTAVGDAIAGQGVHYHLE	301
RESULT 13			
ID	Q8DVL7	PRELIMINARY;	PRT; 304 AA.
AC	Q8DVL7;		
DT	01-MAR-2003	(TrEMBLrel. 23, Created)	
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Putative thioredoxin reductase (NADPH) (EC 1.6.4.5).		
GN	TRXB OR SMU_463.		
OS	Streptococcus mutans.		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI_TaxID=1309;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=UAI59 / ATCC 700610 / Serotype C;		
RX	MEDLINE=22295063; PubMed=12397186;		
RA	Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,		
RA	Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,		
RA	Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;		
RT	"Genome sequence of Streptococcus mutans UAI59, a cariogenic dental		
RT	pathogen.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).		
DR	EMBL; AE014892; AAN58212.1; -.		
DR	GO; GO:0005737; C:cytoplasm; IEA.		
DR	GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.		
DR	GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	GO; GO:0019430; P:removal of superoxide radicals; IEA.		
DR	InterPro; IPR000759; Adrxn reductase.		
DR	InterPro; IPR001327; FAD pyr redox.		
DR	InterPro; IPR000103; Pyridine redox_2.		
DR	InterPro; IPR001100; Pyr_redox.		
DR	InterPro; IPR008255; Pyr_redox2_AS.		
DR	InterPro; IPR005982; Thioredox_reduct.		
DR	Pfam; PF00070; pyr_redox; 1.		
DR	PRINTS; PR00419; ADXRDTASE.		
DR	PRINTS; PR00368; FADPNR.		
DR	PRINTS; PR00411; PNDRDTASEI.		
DR	PRINTS; PR00469; PNDRDTASEII.		
DR	TIGRFAMs; TIGR01292; TRX reduct; 1.		
DR	PROSITE; PS00573; PYRIDINE_REDOX_2; 1.		
KW	Oxidoreductase; Complete proteome.		
SQ	SEQUENCE 304 AA; 33117 MW; CEF7BEC1BE80A50F CRC64;		
Query Match 53.1%; Score 882; DB 16; Length 304;			
Best Local Similarity 55.2%; Pred. No. 1e-54;			
Matches 165; Conservative 52; Mismatches 82; Indels 0; Gaps 0;			
QY	7	FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST	66
DB	2	YDTLIISGPGAGMTAAVYAAARSNSVAIEQAGPGQMNNTSDIENYPGDHISGPELSM	61


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Db 62 ELSMKMAEPLGGLGVENAYGFVTAIEDHGYKKIITDEDFVTKSIIATGANHRKLEIP 121
Qy 123 GEQELGGRGVSYCAVCDGAFKKNKELFVIGGDSAVEGTTTFFADKVTIVHRRDELRA 182
Db 122 GEEYVARGVSYCAVCDGAFKKNKELFVIGGDSAVEGTTTFFADKVTIVHRRDELRA 181
Qy 183 QRIQDRAFNKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSEETHEADGVFTYIGMK 242
Db 182 QEIIQRAFKEKINFWDSPMEIKGDDKKVQSVVYKVKVTGEVTEKAFGGIIFLYVGLD 241
Qy 243 PLTAPFDKLGITNDVGYITVTKDDMTTSVPGIFAGDVRDKGLRQIVTATGDSIAAQSAA 302
Db 242 PVAFAGNLGTDGAGWIIITDHDHRTSLPGIFAVGDRQKDFRQITTAIGDGAQAQEA 301
Qy 303 EYIEHLN 309
Db 302 KFVAELD 308

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RESULT 15

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Q8E773 PRELIMINARY; PRT; 304 AA.
AC Q8E773;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN GBS0284.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaser P., Zusiok C., Buchrieser C., Chevalier P., Frangeul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL: AL766844; CAD45929.1; -.
DR SAGALIST; gbs0284; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019430; P:removal of superoxide radicals; IEA.
DR InterPro; IPR000759; Adrxn reductase.
DR InterPro; IPR001327; FAD pyr redox.
DR InterPro; IPR001033; Pyridine redox_2.
DR InterPro; IPR001100; Pyr redox.
DR InterPro; IPR008255; Pyr_redox2_AS.
DR InterPro; IPR005982; Thioredox_reduct.
DR Pfam; PF00070; pyr_redox; 1.
DR PRINTS; PR00419; ADXRDASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNRDRTASEI.
DR PRINTS; PR00459; PNRDRTASEII.
DR TIGRPFAM; TIGR01292; TRX reduct; 1.
DR PROSITE; PS00573; PYRIDINE REDOX 2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 304 AA; 33123 MW; 4B6B5E55FB84E8D CRC64;

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Query Match 51.3%; Score 852.5; DB 16; Length 304;
Best Local Similarity 53.3%; Pred. NO. 1.3e-52;
Matches 161; Conservative 57; Mismatches 83; Indels 1; Gaps 1;

Qy 7 FDIAGAGPAGMTAAVYASRANKVTVMIEGIPCGQMANTVEENPFPGFEMITGPDLST 66
2 YDTLIIGSGPGGMTAAVYASRANKVTVMIEGIPCGQMANTVEENPFPGFEMITGPDLST 61

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Qy 67 KMFPHAKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIATGAEEKYKIGVPGEOE 126
Db 62 KMYEPELEKFEVEHLYGIQVRVENDGDYKRVITEDSEYAKTVIATGAKNSLLGVPGEE 121
Qy 127 LGEGVSYCAVCDGAFKKNKELFVIGGDSAVEGTTTFFADKVTIVHRRDELRAQRIIL 186
Db 122 YTSRGVSYCAVCDGAFKKNKELFVIGGDSAVEGTTTFFADKVTIVHRRDELRAQRIIL 181
Qy 187 QDRAFNKNDKIDFIWSHTTKSINEXDKGVSVTLTSTKDGSEETHEADGVFTYIGMKPLTA 246
Db 182 QDRAFNKEXFVWDSPMEIKGDDKKVQSVVYKVKVTGEVTEKAFGGIIFLYVGLD 241
Qy 247 PFKDLGITNDVGYITVTKDDMTTSVPGIFAGDVRDKGLRQIVTATGDSIAAQAEEVI - 305
Db 242 MVSELGITDETGWLTDTNMTSIPGLYALGDVVRQKDLRQIATAVGGAIAQGVYNYIT 301
Qy 306 EH 307
Db 302 EH 303

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Search completed: September 15, 2004, 12:20:47
Job time : 118 secs

